## O'Bryen, Barbara

From: Sent:

To:

Zhou, Shubo (AU1631) Wednesday, December 26, 2001 9:55 AM O'Bryen, Barbara

Subject:

search request for 09/422,838

Happy holiday, Barb! Another search for you. Enjoy!

Joe

Shubo "Joe" Zhou, Ph.D. Patent Examiner (703)-605-1158, CM1/12B03 ÀU 1631, US PTO

Search Request

Requester's full name: Shubo "Joe" Zhou

**Examiner #: 78282** 

Art Unit: 1631

**Phone #:** 703-605-1158

Mailbox #: 12D01/CM1

Results format: pape

Room #: 12B03

\*

**Serial #:** 09/422,838

Please search:

Protein databases for

**SEQ ID NO: 33** 

Including:

1. default search

Please provide 45 alignments for the search.

POINT OF CONTACT: **EARB O'BRYEN** TECH. INFORMATION SPECIALIST STIC CM1 12C14 308-4291

12-26-01

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us-09-422-838c-33.rpr

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; Search time 13.48 Seconds (without alignments) 203.434 Million cell updates/sec
                                                                                                                                                                                                                           1 IEGPTLRQWLAARAGGGCGGGGIEGPTLRQWLAARA 36
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                         219241 seqs, 76174552 residues
                                                                                                           December 26, 2001, 10:26:08
                                                                       OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                 BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                               US-09-422-838C-33
197
                                                                                                                                                                                     Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                 Scoring table:
                                                                                                                                                                                                                                                                                                                         Searched:
                                                                                                           Run on:
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219241

Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000

Minimum DB seq Maximum DB seq

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 100 summaries PIR\_68:\*
1: pirl:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		ď			SUMMARIES	
Result No.	Score	Query Match	& Query Match Length	DB	ID	
7	67	34.0	865	~	T34584	probable secreted
2	63.5	32.2	209	7	268	Q
m	60.5	30.7	210	7	A42687	pr
4	9	0	200	7	T20961	ч
5	59.5	0	518	7	872938	
9	59	29.9	683	7	B71325	rved hypc
7	58	29.4	302	7	S71334	acetyl xylan ester
8	58		924	7	E71476	alaninetRNA liga
6	57.5	29.5	495	7	D70505	probable HflX - My
10	57	28.9	339	7	S20880	eir
11			77	~	INSH	
12	56.5	28.7	105	Н	IPBO	insulin precursor
13		28.7	176	7	B72698	hypothetical prote
14	26	28.4	56	7	T12783	sublancin 168 prec
15	26	28.4	163	7	T33130	
16	99	28.4	349	7	E86405	
17	26	28.4	510	7	S41943	4
18	99	28.4	511	7	S44716	1,4
19	26	28.4	540	7	S41942	cellulose 1,4-beta
20	26	28.4	619	7	KSNCLO	$\overline{}$
21	26	28.4	619		KSNCLT	laccase (EC 1.10.3
22	26	28.4	767	7	E70895	hypothetical glyci
23	55	27.9	180	7	T49530	6
24	55	27.9	201	7	T49792	
25	52	27.9	257	7	C84890	_
26		7.	331	7	T26807	hypothetical prote
27		7	333	7	T26808	
28	52	27.9	393	7	026	thetical
29		27.9	399	7	T47712	MYB transcription

numb protein - fru alanyl-tRNA synthe probable lsr2 prot dnaK type molecula Ul-snRNP binding p DNA-binding protei ovo protein - frui hypothetical 20.2k transcription fact probable amidase - coenzyme F420 hydr potbable amidase - potbable Ul small hypothetical prote probable Ul small hypothetical prote	CREB-binding prote glycine-rich prote transcription fact spheroidin precurs probable succinyl-70K UI small nucle subtliisin-like pr transcription fact subtliisin-like pr transcription fact subtliisin-like pr hypothetical prote hypothetical prote hypothetical prote subtliisin-like pr subtliisin-like pr subtliisin-like pr subtliisin-like pr subtliisin-like pr hypothetical prote homeotic protein s hypothetical prote corposed	myosin heavy chain nitrite reductase hypothetical prote transcription fact UI snRNP 70K prote UI snRNP 70K prote UI snRNP 70K prote protain-tyrosine k hypothetical prote probable glycine-r hypothetical prote ankyrin 3 homolog probable membrane hypothetical prote splicing factor SF UTP-9lucose-1-photransforming prote hypothetical protein e glutamyl-tRNA(Gln) probable farnesyl
000000000000000000000000000000000000000	7 113828 5 2 7448968 2 2 7478328 2 2 7478328 2 2 7478328 4 2 7478328 4 2 7478328 5 2 7478328 6 2 8394491 7 2 747856 8 1 747856 9 2 747856 9 3 2 747856 9 4 2 747856 9 5 2 747856 9 5 2 747856 9 6 2 747856 9 6 2 747856 9 7 7 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	
555 27.9 87.7 1191 201 201 201 201 201 201 201 201 201 20	55. 5. 5. 5. 5. 5. 5. 5. 5. 5. 5. 5. 5.	52 26.4 116 52 26.4 117 52 26.4 117 53 26.1 37 55 26.1 37 55 26.1 47 61 25.9 100 61 25.9 28 61 25.9 28 61 25.9 30 61 25.9 38 61 25.9 38 61 25.9 38 61 25.9 48 61 25.9 48
		5 5 7 1 1 2 2 2 1 1 2 2 2 1 1 2 2 2 1 1 2 2 2 1 1 2 2 2 1 1 2

us-09-422-838c-33.rpr

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C; Species: Homo sapiens (man)
C; Date: 31-Dec-1993 #text_change 16-Jul-1999
C; Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 16-Jul-1999
C; Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 16-Jul-1999
C; Accession: A42687; JH0503
B; IP, N.Y.; Ibanez, C.F.; Nye, S.H.; McClain, J.; Jones, P.F.; Gies, D.R.; Belluscio, Proc. Natl. Acad. Sci. U.S.A. 89, 3060-3064, 1992
A; Title: Mammalian neurotrophin-4: structure, chromosomal localization, tissue distrints. As Accession: A42687; MUID:92212967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A.Cross-references: GB:M86528; NID:g190264; PIDN:AAA60154.1; PID:g190265
A;Note: sequence extracted from NCBI backbone (NCBIN:93810, NCBIP:93811)
R:Berkemeier, L.R.; Winslow, J.W.; Kaplan, D.R.; Nikolics, K.; Goeddel, D.V.; Rosenth
Neuron 7, 857-866, 1991
A;Title: Neurotrophin-5: a novel neurotrophic factor that activates trk and trkB.
A;Reference number: JH0503; MUID:92075279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Residues: 1-210 <BER>
C;Comment: The neurotrophins stimulate autophosphorylation and transduce signals thro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Cross-references: EMBL: Z78013; PIDN: CAB01420.1; GSPDB: GN00023; CESP: F15B9.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 C;Accession: T20961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C.Superfamily: nerve growth factor beta chain
C.Keywords: glycoprotein
C.Reywords: glycoprotein
F: 1-24/Domain: signal sequence #status predicted <SIG>
F: 25-80/Domain: propeptide #status predicted <PRO>
F: 81-210/Product: neurotrophin-4 #status predicted <NEU>
F: 76/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ch 30.7%; Score 60.5; DB 2; Length 210; 1 Similarity 35.0%; Pred. No. 6.9; 14; Conservative 3; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 60; DB 2; Length 500;
Pred. No. 17;
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128 GSPLRQYFFETRCKAESAGEGGPGVGGGGCRGVDRRHWLS 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         129 GSPLRQYFFETRCKADNAEEGGPGAGGGCCRGVDRRHWVS 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein F15B9.5 - Caenorhabditis elegans C;Species: Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 GPTLRQWL-----AARAGGGGGGGGGEGPTLRQWLA 33
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A;Molecule type: DNA
A;Residues: 1-500 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         submitted to the EMBL Data Library, August 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Gene: GDB:NTF5
A;Cross-references: GDB:134723; OMIM:162662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Experimental source: clone F15B9
                                                                                                                                                                                                                       N;Alternate names: neurotrophin-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30.5%;
ilarity 52.2%;
Conservative
                                                                                                                                                                                     neurotrophin-4 precursor - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Map position: 19pter-19qter
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A; Accession: T20961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-210 <IP1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 14; Conserv
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Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-210 <BER>
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                                                                                                             RESULT
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A; Residues: 1-209 <-BER>
A; Residues: 1-209 <-BER>
A; Residues: 1-70; Fy. 178-209 <-BER|>
A; Molecule type: DNA
A; Residues: 1-70; Fy. 178-209 <-BER|>
A; Molecule type: mRNA
A; Residues: 1-77; Fy. 178-209 <-BER|>
A; Cross references: GB:S69323; NID:g40025; PIDN:AAB20548.1; PID:g240026
A; Cromment: This protein is a targed-derived, diffusible neurotrophic factor.
C; Comment: The neurotrophins stimulate autophosphorylation and transduce signals through
C; Superfamily: nerve growth factor beta chain
C; Superfamily: nerve growth factor beta chain
C; Superfamily: nerve growth factor perdicted <-SIG>
F; T20/Domain: signal sequence #status predicted <-RGO>
F; 21-79/Domain: propeptide #status predicted <-RGO>
F; 80-209/Product: neurotrophin-5 #status predicted <-RGO>
F; 75/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C:Species: Rattus norvegicus (Norway rat)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 16-Jul-1999
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 16-Jul-1999
C:Caccession: B42687; JH0504; JH0505
R:IP, N.Y.: Ibanez, C.F.: Nye, S.H.: McClain, J.; Jones, P.F.; Gies, D.R.; Belluscio, L. Proc. Natl. Acad. Sci. U.S.A. 89, 3060-3064, 1992
A:Title: Mammalian neurotrophin-4: structure, chromosomal localization, tissue distribut A:Accession: B42687
A:Accession: B42687
A:Accession: Preliminary
A:Status: preliminary
A:Status: preliminary
A:Residues: 1-209 <IPA>
A:Residues: 1-209 <IPA>
A:Residues: 1-209 <IPA
A:Cross-references: GB:M86742; NID:g205775; PIDN:AAA41728.1; PID:g205776
A:Cross-references: GB:M86742; NID:g205775; PIDN:AAA41728.1; A:Bockendeler, L.K.; Winslow, J.W.; Kaplan, D.R.; Nikolics, K.; Goeddel, D.V.; Rosenthal, Neuron 7, 857-866. 1991
A:Title: Neurotrophin-5: a novel neurotrophic factor that activates trk and trkB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Cross-references: EMBL: ALO21529; PIDN: CAA16449.1; GSPDB: GN00070; SCOEDB: SC10A5.17
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                                                                                                                                                                                                                    Species: Streptomyces coelicolor
Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 24-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                        C;Accession: T34584
R;Murphy, L.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, January 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 865;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Indels
                                                                                                                                                                              probable secreted proteinase - Streptomyces coelicolor
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                                                                                                                                                                                                                                                                                                                                                                                              A;Reference number: 221548
A;Accession: T34584
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-865 < MUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4.6;
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ALIGNMENTS
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Pred. No.
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C; Genetics:
A; Gene: SCOEDB:SCI0A5.17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34.0%;
66.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 66.7'
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              neurotrophin-4 precursor - rat
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Best Local Similarity
Matches 15; Conserv
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C; Species: Chlamydia trachomatis
C; Species: Chlamydia trachomatis
C; Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 08-Oct-1999
C; Accession: E71476
C; Accession: E71476
A; Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia the A; Recence number: A71570; MUID: 99000809
A; Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia the A; Accession: E71476
A; Accession: E71476
A; Maccession: E71476
A; Maccession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C. Accession: D70505
R. Cole, S.T. Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon R. Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon R. Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A.;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A.;Reference number: A70500; MUID:98295887
A.;Reference number: A70500; MUID:98295887
A.;Stellin, B.G. A.; A70500; MUID:98295887
A.;Stellin, R. Completing the biology of Squence not shown; translation not shown
R;Margolles-Clark, E.; Tenkanen, M.; Soederlund, H.; Penttilae, M.

Sur. J. Biochem. 237, 553-560, 1996
A;Title: Acetyl xylan esterase from Trichoderma reesei contains an active-site serine
A;Reference number: S71334; MUID:96235218
A;Steference number: S71334
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 8
E71476
alanine--tRNA ligase (EC 6.1.1.7) - Chlamydia trachomatis (serotype D, strain UW3/Cx)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   probable Hflx - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 02-Sep-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-302 < MAR>
A; Cross-treferences: EMBL: 269256; NID:91431619; PID:e220701; PID:91431620
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8; Indels 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A.Gene: alas
C.Superfamily: alanine--tRNA ligase
C.Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Gene: axel
C; Superfamily: fungal cellulose-binding domain homology
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-302/Product: acetyl xylan esterase #status predicted <WAT>
F;271-302/Pomain: fungal cellulose-binding domain homology <FCB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 29.4%; Score 58; DB 2; Length 302; Best Local Similarity 35.9%; Pred. No. 18; Matches 14; Conservative 1; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               874 VOAHTLIAELLAPYGGRCGGKAISAQGSSAELPQIEFLNKTLROWISTQ 922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2; Length 924;
47;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              265 GPTQTHW-----GQCGGQGWTGPTQCESGTTCQVISQW 297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29.4%; Score 58; 30.6%; Pred. No.
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Best Local Similarity 30.69
Matches 15; Conservative
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C:Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C:Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C:Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 05-Nov-1999
C:Accession: B71325
R:Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin ston, J.; Rhalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McDc they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:AE001220; GB:AE000520; NID:g3322705; PIDN:AAC65409.1; PID:g332270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Start codon: GTG
C;Superfamily: GTP-binding protein hflX; translation elongation factor Tu homology
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A;Accession: B71325
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C;Species: Trichoderma reesei
C;Date: 23-Jul.1997 #sequence_revision 01-Aug-1997 #text_change 17-Mar-1999
C;Accession: S71334
                                                                                                                                                                                                                                                                                                                                                                                                                     N;Alternate names: B2235_C2_202 protein
C;Species: Mycobacterium leprae
C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 23-Mar-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: DNA
A;Residues: 1-518 <SMI>
A;Cross-references: EMBL:U00019; NID:g467079; PIDN:AAA17274.1; PID:g467091
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Smith, D.R.; Robison, K. submitted to the EMBL Data Library, November 1993 A;Description: Mycobacterium leprae cosmid B2235. A;Reference number: $72587 A;Recession: $72938 A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Mismatches
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Pred. No. 19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        219 PRLRGWGESMSRQVGGRAGGSGGGVGLRGP 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 PTLRQW-----LAARAGGGCGGGGIEGP 26
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                                                                                                                   429 GSMLGRFLSNRGGGGGGGGGGGG 451
                                                                3 GPTLRQWLAARAGGGCGGGGIEG 25
                                                                                                                                                                                                                                                                                                                                                                                hflX protein - Mycobacterium leprae
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Best Local Similarity 43.8%;
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Best Local Similarity
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A; Residues: 1-683 <COL>
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Matches
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S71334
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Conservative
                       60, 556-565, 1955
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A; Accession: A90342
A; Molecule type: protein
                                                                                                                                                                                                         A; Molecule type: protein
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Matches 13; Conserv
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A; Residues: 1-339 < RENS
A; Cross-retences: EMBL: X62669; NID:951414; PIDN:CAA44542.1; PID:951416
A; Duboule, D.; Dolle, P.
EMBO J. 8, 1497-1505, 1989
A; Title: The structural and functional organization of the murine HOX gene family resemb
A; Reference number: S09569; MUID:89356621
A;Residues: 1-495 <COL>
A;Cross_references: GB:Z98209; GB:AL123456; NID:93261838; PIDN:CAB10901.1; PID:e332282;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 16-Sep-1992 #sequence_travision 16-Sep-1992 #text_change 17-Nov-2000
C;Accession: 820880; 809569; 809398
R;Renucci, A.; Zappavigna, V.; Zakany, J.; Izpisua-Belmonte, J.C.; Buerki, K.; Duboule, Margo J. II, 1452-1468, 1992
A;Title: Comparison of mouse and human HOX-4 complexes defines conserved sequences invol.
A;Reference number: $20879; MUID: 92224884
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A/Reference number: S09398; MUID:89356622
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A;Residues: 272-331 <DOL>
A;Cross-references: GB:X14714; GB:M21040; NID:g51427; PIDN:CAB57813.1; PID:g6015583
                                                                                                                                                                             A;Gene: hflx
C;Superfamily: GTP-binding protein hflx; translation elongation factor Tu homology
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C;Datte: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 16-Jul-1999
C;Accession: Si6430; Si6431
R;Brown, H.; Sanger, F.; Kitai, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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C;Superfamily: unassigned homeobox proteins; homeobox homology
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;273-329/Domain: homeobox homology <HOX>
                                                                                                                                                                                                                                                                                                                                                                                  Length 495;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                             DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                             Score 57.5; 1
Pred. No. 31;
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A; Residues: 272-331 < DUB>
A; Cross references: EMBL:X14714; NID:951427;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 GPTLRQWL-----AARAGGGCGGGGIEGP 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 PTLROW-----LAARAGGGCGGGGIEGP 26
                                                                                             A; Experimental source: strain H37Rv C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                    29.2%;
ilarity 43.3%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             homeotic protein Hox 4.5 - mouse
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Best Local Similarity
Matches 13; Conserv
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C;Genetics:
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A;Residues: 1-30;57-77 <BRO>
R;Peterson, J.D.; Nehrlich, S.; Oyer, P.E.; Steiner, D.F.
J. Biol. Chem. 247, 4866-4871, 1972
A;Title: Determination of the amino acid sequence of the monkey, sheep, and dog proin A;Reference number: A92111: MUID:72258016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Insulin precursor - bovine
C;Species: Bos primigenius taurus (cattle)
C;Species: Bos primigenius taurus (cattle)
C;Date: 24-Apr-1984 #sequence_revision 22-Apr-1995 #text_change 16-Jul-1999
C;Date: 24-Apr-1984 #sequence_revision 22-Apr-1995 #text_change 16-Jul-1999
C;Accession: A40909; A92080; A92074; A91185; A90342; A90341; S48184; S48185; S46258;
R;D'Agostino, J; Younes, M.A.; White, J.W.; Besch, P.K.; Field, J.B.; Frazier, M.L.
Mol. Endocrinol: 1, 327-331, 1987
A;Title: Cloning and nucleotide sequence analysis of complementary deoxyribonucleic a
A;Reference number: A40909; MUID:88288209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eur. J. Biochem. 20, 183-189, 1971
A.Title: Bovine proinsulin: amino acid sequence of the C-peptide isolated from pancre A. Reference number: A91185; MUID:71257721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Residues: 57-82 <SAL>
R; Sanger, F.; Thompson, E.O.P.
Blochem. J. 53, 366-374, 1953
A; Title: The amino-acid sequence in the glycyl chain of insulin. 2. The investigation
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R: Steiner, D.F.; Cho, S.; Oyer, P.E.; Terris, S.; Peterson, J.D.; Rubenstein, A.H.
B. A. Chem. 246, 1365-1374, 1971
A; Title: Isolation and characterization of proinsulin C-peptide from bovine pancreas.
A; Reference number: A92074; MUID: 71116409
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A; Residues: 1-105 <DAA>
A; Cross-references: GB: M54979; NID:g163578; PIDN:AAA30722.1; PID:g163579
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R; Nolan, C.; Margoliash, E.; Peterson, J.D.; Steiner, D.F.
Biol. Chem. 246, 2780-2795, 1971
A; Title: The structure of bovine proinsulin.
A; Reference number: A92080; MUID:71166442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C. Superfamily: insulin

C. Keywords: hormone, pancreas

F:1-30,777/Product: insulin #status experimental <BCH>

F:1-30,577/Product: insulin #status experimental <MAT>

F:31-56/Domain: connecting peptide #status experimental <

F:57-77/Domain: insulin chain A #status experimental <ACH>

F:7-63,19-76,62-67/Disulfide bonds: #status predicted
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A; Residues: 57-82 <STE>
R; Salokangas, A.; Smyth, D.G.; Markussen, J.; Sundby, F.
Eur. J. Blochem. 20, 183-189, 1971
A; Title: The structure of pig and sheep insulins.
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2; Mismatches
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1;

19; . Gaps

8; Indels

Pred. No. 16;

-GGGGIEGPTLRQ 30

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34.98;
                                Conservative
Best Local Similarity
Matches 15; Conserv
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A; Residues: 1-56 <KUN>
                                                                                                7 ROWLAARAGGGC
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                                   Matches
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awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K
DNA Res. 6, 83-101, 1999
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A; Status: preliminary
A; Modecule type: DNA
A; Residues: 1-176 < KAW>
A; Cross-references: DDBJ:AP000060; NID:95104188; PIDN:BAA79986.1; PID:d1043772; PID:9510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Wenzel, T.; Eckerskorn, C.; Lottspeich, F.; Baumeister, W.
FEBS Lett. 349, 205-220; 1994
A;Title: Existence of a molecular ruler in proteasomes suggested by analysis of degradat
A;Reference number: S46258; MUID:94326921
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A:Reference number: A72450; MUID:99310339
                                   R;Sanger, F.; Tuppy, H.
Biochem. J. 49, 481–490, 1951
A;Title: The amino-acid sequence in the phenylalanyl chain of insulin. 2. The investigat
                                                                                                                                                                                                                                                                                                               A;Title: Site-specific oxidation of histidine residues in glycated insulin mediated by A;Reference number: S48184; MUID:9433378
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C.Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
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F;1-24/Domain: signal sequence #status predicted <SIG>
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ilarity 50.0%; Pred. No. 10;
Conservative 2; Mismatches
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A; Residues: 25-30, X', 32-42, X', 44-54 <CH2>
R; Ryle, A.P.; Sanger, F.; Smith, L.F.; Kitai,
R; Ryle, A.P.; Sanger, P.; Smith, L.F.; Kitai,
A; Title: The disulphide bonds of insulin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Reference number: A90343
A; Contents: annotation; amides; disulfides
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                                                                                                                                                                                                                                                     R;Cheng, R.; Kawakishi, S.
Eur. J. Biochem. 223, 759-764, 1994
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                                                                                                                             A; Reference number: A90341
                                                                                                                                                                                              A; Molecule type: protein A; Residues: 25-54 <SA2>
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A; Residues: 25-54 <WEN>
         A; Residues: 85-105 <SAN>
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Best Local Similarity
Matches 13; Conserv
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A; Reference number: 217583
A; Accession: T12783
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A; Accession: T12783
A; Accession: T12783
A; Molecule type: DNA
A; Residues: 1-56 < LAZ>
A; Molecule type: DNA
A; Residues: 1-56 < LAZ>
A; Cross-references: EMBL:AP020713; NID:g3025478; PID:g3025497; PIDN:AAC12992.1
A; Cross-references: EMBL:AP020713; NID:g3025478; PID:g3025497; PIDN:AAC12992.1
A; Runst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber A; Cross-references: EMBL:AP020713; NID:g3025478; PID:gabano, V.; Carter, N.M.; Albert, S.; Brouilet, S.; Bruschi, C.V.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, Nature 390, 249-256, 1997
A; Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galizzi, A; Hullo, M.; Rocter, T.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.; Nothors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau, V., M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portete A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Se akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiya A; Authors: Yoshikawa, H.; Danchin, A.; Tosato, V.; Uchiya A; Althors: Yoshikawa, H.; Danchin, A.; Tanaka, A; Hille: The complete genome sequence of the Gram-positive bacterium Bacillus subtili
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A)Cross-references: GB:299115, GB:AL009126; NID:g2634478; PIDN:CAB14066.1; PID:e11835 A)Expositionental source: strain 168 C;Genetics: <LA1> A)Gene: yolg C;Genetics: <KU1>
                                                                                                                                                                                                                      sublancin 168 precursor - Bacillus subtilis phage SPBc2
C;Species: Bacillus subtilis phage SPBc2
C;Accession: 112783; H69719
R;Lazarevic, V; Duesterhoeft, A.; Soldo, B.; Hilbert, H.; Mauel, C.; Karamata, D. submitted to the EMBL Data Library, August 1997
A;Description: The complete nucleotide sequence of the Bacillus subtilis Spbetac2 pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A/Gene: sunA
C; Superfamily: unassigned lanthionine-containing peptides
C; Superfamily: antiblotic; lanthionine
C; Keywords: antiblotic; lanthionine
C; Keywords: antiblotic; lanthionine
F; 10-56/Product: sublancin 168 #status predicted <MAT>
F; 20-56/Product: sublancin 168 #status predicted <MAT>
F; 20-56/Prolaulfide bonds: #status experimental
F; 33-48/Disulfide bonds: #status predicted
F; 33-Modified site: dehydroalanine (Ser) #status experimental
F; 38-41/Cross-link: (2S, 3S, 6R)-3-methyl-lanthionine (Thr-Cys) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein C23H5.9 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequencc_revision 29-Oct-1999 #text_change 29-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2; Length 56; 6.7;
ROGLHGEEGGGCDCKGCGRRLNPPPPGHHWQGGGGEEGEELRR 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28.4%; Score 56; 44.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9 WLAARAGG--GCGGGGIEGPTLRQW 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30 WLOCASGGTIGCGGGAVACONYROF 54
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Best Local Similarity 44.0'
Matches 11; Conservative
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Query Match

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Query Match
Best Local Similarity 48.0°
Matches 12; Conservative
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Best Local Similarity
Matches 12; Conserv
        A; Residues: 1-510 <S12>
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Cyaces: Or Target 2. 2001 #Sequence_revision UZ-Mar-2001 #text_change 31-Mar-2001
Chaccasion: E86405
R:Theologis, A.: Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, ansen, N.F.; Hughes, B.; Huizar, L.
Rature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Reterence number: A86141; MUID:21016719
A;Reterence number: A86141; MUID:21016719
A;Reterence by Arabidopsis.
A;Residues: 1-349 <STO>
A;Residues: BNA
A;Residues: 1-349 <STO>
A;Residues: Lidianary
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S41943
S41943
S41943
S41944
Spleidose 1,4-beta-cellobiosidase (EC 3.2.1.91) - basidiomycete (Phanerochaete chrysospot C;Speidose 1,4-beta-cellobiosidase (EC 3.2.1.91) - basidiomycete (Phanerochaete chrysospot Spleidose 1,4-beta-cellobiosidate chrysospot in Satoria 1994 #sequence_revision 10-Nov-1995 #text_change 22-Jun-1999
S,Accession: 844715; 8441943
Mol. Microbiol. 12, 209-216, 1994
A;Title: Differential expression of multiple exo-cellobiohydrolase I-like genes in the 1 A;Reference number: S44714; MUID: 94335641
A;Reference number: S44715
A;Molecule type: mRNA
                                                                                                                                                              A:Status: preliminary; translated from GB/EMBL/DDBJ
A;Nolcoule type: DNA
A;Rosidues: 1.163 <LAM>
A;Cross-references: EMBL:AF067609; PIDN:AAC17537.1; GSPDB:GN00022; CESP:C23H5.9
A:Experimental source: strain Bristol N2; clone C23H5
A;Genetics:
A;Gene: CESP:C23H5.9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 56; DB 2; Length 163; Pred. No. 17; 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 349;
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                    R;Lamar, E.; Kramer, J. submitted to the EMBL Data Library, May 1998 A;Description: The sequence of C. elegans cosmid C23H5. A;Reference number: 221286 A;Reference number: T33130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5
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Pred. No. 33;
1; Mismatches
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33;
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Best Local Similarity 75.0
Matches 12; Conservative
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Best Local Similarity 66.7
Matches 10; Conservative
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A;Introns: 1/3; 101/3; 126/2
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C; Accession: T33130
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A;Introns: 201/3; 506/1
C;Superfamily: cellulose 1,4-beta-cellobiosidase I; fungal cellulose-binding domain h
C;Keywords: glycosidase; hydrolase; polysaccharide degradation
F;480-511/Domain: fungal cellulose-binding domain homology <FCB>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cellulose 1,4-beta-cellobiosidase (EC 3.2.1.91) - basidiomycete (Phanerochaete chryso C;Species: Phanerochaete chrysosporium
C;Date: 20-0ct-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jul-2000
                            C;Genetics: 805/1
A;Introns: 505/1
C;Superfamily: cellulose 1,4-beta-cellobiosidase I; fungal cellulose-binding domain
C;Reywords: glycosidase; hydrolase; polysaccharide degradation
E;479-510/Domain: fungal cellulose-binding domain homology <FCB>
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C;Superfamily: cellulose 1,4-beta-cellobiosidase I; fungal cellulose-binding domain
C;Keywords: glycosidase; hydrolase; polysaccharide degradation
F;479-510/Domain: fungal cellulose-binding domain homology <FCB>
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A; Cross-references: BMBL: 222527; NID: 9296028; PIDN: CAA80252.1; PID: 93980202 C; Genetics:
A:Cross-references: EMBL:Z29653; NID:g453222; PIDN:CAA82762.1; PID:g453224
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                                                                                                                                                                                                                                                                                       Length 510;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2; Length 511;
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1; Mismatches
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F;22-49/Domain: propeptide #status predicted <PRO>
F;50-619/Product: laccase #status predicted <MAT>
F;84-15/Domain: aminor-terminal beta-barrel #status predicted <BB1>
F;84-15/Domain: middle beta-barrel #status predicted <BB2>
F;431-580/Domain: carboxyl-terminal beta-barrel #status predicted <BB3>
F;139-282.295;340,422.444/Apinding site: carbohydrate (Asn) (covalent) #status predict F;144.480/Binding site: copper (His) (type 2) #status predicted F;146.189,131,482,548.550/Binding site: 2Cu O cluster (His) (copper type 3) #status predicted F;147.549,554/Binding site: Copper (His, Cys, His) (type 1) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Date: 02-Un-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000 C;Date: 02-Un-2000 #sequence_revision 02-Jun-2000 #sequence_revision 02-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical glycine-rich protein Rv1087 - Mycobacterium tuberculosis (strain H37RV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            related to glycine-rich cell wall structural protein [imported] - Neurospora crassa N;Alternate names: protein B21J21.90
C;Spec:es: Neurospora crassa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:AL355929; GSPDB:GN00116; NCSP:B21J21.90 A;Experimental source: BAC clone B21J21; strain OR74A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28.4%; Score 56; DB 2; Length 767; 46.7%; Pred. No. 66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 56; DB 1; Length 619;
Pred. No. 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           681 GPTNFGLNGAGGGGGGGGGGTGP----WL 706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 GPTLRQWLAARAGGGCGGGGIEGPTLRQWL 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44 AERYGGG-GGGCUSPINRQCW 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene: Rv1087
C;Superfamily: unassigned collagens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11 AARAGGGGGGGGIEGPTLRQ-W 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Experimental source: strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match 28.4
Best Local Similarity 46.7
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 63.6
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Resignes: 1-180 <SCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Gene: NCSP: B21J21.90
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A; Status. preliminary
A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genetics:
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Nathernate names: urishiol oxidase
C; Alternate names: urishiol oxidase
C; Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 11-Jun-1999
C; Accession: B28523
C; Accession: B28523
R; Germann, U.A.; Mueller, G.; Hunziker, P.E.; Lerch, K.
J. Biol. Chem. 263, 885-896, 1988
A; Title: Characterization of two allelic forms of Neurospora crassa laccase. Amino- and A; Accession: B28523
A; Molecule type: DNA
A; Residuas: 1-619 < GER>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Keywords: copper, glycoprotein; oxidoreductase
C;Keywords: copper, glycoprotein; oxidoreductase
E;12-17Domain: signal sequence *status predicted <SIG>
E;12-17Domain: signal sequence *status predicted <>ROPO>
F;20-49/Domain: propeptide *status predicted <MATP
E;84-215/Domain: midlo-terminal beta-barrel *status predicted <BB2>
F;16-372/Domain: midlo-terminal beta-barrel *status predicted <BB2>
F;43-680/Domain: carboxyl-terminal beta-barrel *status predicted <BB3>
F;139,282,295,340,422,444/Feinding site: carbohydrate (Asn) (covalent) *status predicted F;144,480/Sidhing site: copper (His) (type 2) *status predicted F;146,189,191,482,548 550/Einding site: 2Cu-0 cluster (His) (type 1) *status predicted F;747,549,554/Einding site: copper (His, Cys, His) (type 1) *status predicted
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C;Comment: This enzyme, which catalyzes the oxidation of benzendiol to benzosemiquinone
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                         C; Species: Neurospora crassa
C, Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 11-Jun-1999
C; Accession: A28523; A29762
R; Germann, U.A.; Mueller, G.; Hunziker, P.E.; Lerch, K.
B; Biol. Chem. 263, 886-896, 1988
A; Title: Cheracterization of two allelic forms of Neurospora crassa laccase. Amino- and A; Reference number: A28523; MUID:88087214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Wolecule type: DNA
A;Residues: 379-619 (GEE2>
A;Cross-references: GB:M14554; NID:g168823; PIDN:AAA33590.1; PID:g168824
C;Comment: This enzyme, which catalyzes the oxidation of benzendiol to benzosemiquinone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rigermann, U.A.; Lerch, K. Parock, K. Parock, R. Proc. Natl. Acad. Sci. U.S.A. 83, 8854-8858, 1986
Aritile: Isolation and partial nucleotide sequence of the laccase gene from Neurospora A; Reference number: A29762; MUID:87067412
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Pred. No. 55;
                                                                                                                                                                                                                                                                                                    laccase (EC 1.10.3.2) precursor – Neurospora crassa (strain OR)
N;Alternate names: urishiol oxidase
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                                 473 GPTVPOW-----GOCGGIGYSGST 491
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A;Residues: 1-619 <GER>
A;Cross-references: EMBL:M14554
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nes 14; Conserv
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C,Superfamily: laccase
C,Keywords: copper; qly
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-393 <WIL>
A;Cross-references: EMBL:277655; PIDN:CAB01137.1; GSPDB:GN00023; CESP:C56A3.1
A;Experimental source: clone C56A3
C;Genetics:
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 16-Feb-2001
C;Accession: T26807
R;Steward, C.
submitted to the EMBL Data Library, October 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein Y41C4A.4b - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct_1999 #sequence_revision 15-Oct-1999 #text_change 16-Feb-2001
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T20268
                                                                                                                                                                                                                                                                                                 A;Residues: 1-331 <WIL>
A;Cross-references: EMBL:AL032627; PIDN:CAB54381.1; CESP:Y41C4A.4a
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A;Experimental source: clone Y41C4A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 331;
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                                                                                                                                                                                                                                 A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27.9%; Score 55; DB 2; 69.2%; Pred. No. 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-333 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                           A;Gene: CESP:Y41c4A.4a
A;Introns: 24/3; 50/2; 81/3; 159/1; 228/1; 292/3
C;Superfamily: fos/jun DNA-binding domain homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Gene: CESP:Y41c4A.4b
A; Introns: 24/3; 50/2; 81/3; 161/1; 230/1; 294/3
C; Superfamily: fos/jun DNA-binding domain homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Steward, C.
submitted to the EMBL Data Library, October 1998
A;Reference number: 220269
A;Accession: T26808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 55; DB 2
Pred. No. 41;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            submitted to the EMBL Data Library, July 1996
                                                                                                                                                                                                                                                                                                                                                                 A; Experimental source: clone Y41C4A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27.9%;
69.2%;
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Best Local Similarity 69.20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 69.2
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  167 GGGGGGGVPGPS 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ||| ||||: ||:
169 GGGGGGGVPGPS 181
                                                                                                                                                                 A; Reference number: 220269
A; Accession: T26807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15 GGGGGGGIEGPT 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15 GGGGGGGGIEGPT 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Reference number: Z19244
A; Accession: T20268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Accession: T26808
                                                                                                                                                                                                                                                                                                                                                                                            C; Genetics:
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Efficación: Freliminary
Efficación: T49792
Effica
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                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Neurospora crassa
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000
                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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0
                                 Length 180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27.9%; Score 55; DB 2; Length 201; 52.4%; Pred. No. 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27.9%; Score 55; DB 2; Length 257; 81.8%; Pred. No. 33;
                                                                                                 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Indels
                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein B9J10.290 [imported] - Neurospora crassa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein Y41C4A.4a - Caenorhabditis elegans
                          Score 55; DB 2;
Pred. No. 24;
0; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74 RGGGGGGGCGVNG----RWSA 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13 RAGGGGGGGIEGPTLRQWLA 33
                       Ouery Match 27.9%;
Best Local Similarity 73.3%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 27.9
Best Local Similarity 52.4
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                       12 ARAGGGGGGGGIEGP 26
                                                                                                                                                                                                                    58 ADAGGGAGGGGGGP 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15 GGCGGGGIEG 25
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Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Gene: NCSP: B9J10.290
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RESULT 25

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A; Map position: 6

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Gaps

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A; Gene: At2945420 A; Map position: 2

Query Match

RESULT 26

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C; Accession: H81739
R; Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hicke, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzbe, Nucleic Acids Res. 28, 1397-1406, 2000
A; Title: Genome Sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39 A; Reference number: A81500; MUID:2015025
A; Status: preliminary
A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Residues: 1-875 <TET>
A;Cross-references: GB:AE002279; GB:AE002160; NID:97190148; PIDN:AAF39003.1; PID:9719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             probable lsr2 protein - Mycobacterium tuberculosis (strain H37RV)
C:Species: Mycobacterium tuberculosis
C:Decies: Mycobacterium tuberculosis
C:Decies: Ng. 1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C:Accession: F70954
R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Titler Deciphering the biology of Mycobacterium tuberculosis from the complete geno A;Accession: F70954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A:Cross-references: GB:295557; GB:AL123456; NID:93242276; PIDN:CAB08947.1; PID:921139
A:Experimental source: strain H37Rv
C:Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
                                                                                                                        alanyl-tRNA synthetase TC0125 [imported] - Chlamydia muridarum (strain Nigg) C;Species: Chlamydia muridarum, Chlamydia trachomatis MoPn C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-May-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     dnaK-type molecular chaperone - fluke (Schistosoma japonicum) (fragment)
N;Alternate names: heat shock protein 70
C;Species: Schistosoma japonicum
C;Species: Schistosoma japonicum
C;Date: 15-Oct-1994 #sequence_revision 15-Oct-1994 #text_change 20-Aug-1999
C;Accession: A54507
K:Hedstrom, R.; Culpepper, J.; Schinski, V.; Agabian, N.; Newport, G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27.9%; Score 55; DB 2; Length 875; 28.6%; Pred. No. 95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 IEGPTLRQWLAARAGGGCGGGGIE------GPTLRQWLAAR 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 LRQWLAA-----RAGGGCGGGGI---EGPTLRQW 31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Experimental source: strain Nigg (MoPn)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Gene: TC0125
C;Superfamily: alanine--tRNA ligase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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                                                                       31
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                numb protein - fruit fly (Drosophila melanogaster)

(Species: Drosophila melanogaster

(Species: 21-Oct-1992 #sequence_revision 21-Oct-1992 #text_change 24-Sep-1998

(Stacession: A32466

R;Uemura, T.; Shepherd, S.; Ackerman, L.; Jan, L.Y.; Jan, Y.N.

(Cell 58, 349-360, 1989

A;Title: numb, a gene required in determination of cell fate during sensory organ format A;Reference number: A32466; MUID:89324081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C:Accession: 147712
C:Accession: 147712
R:Benes, V.; Wurmbach, E.; Drzonek, H.; Ansorge, W.; Mewes, H.W.; Lemcke, K.; Mayer, K.E
submitted to the Protein Sequence Database, March 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Introns: 113/1
A;Note: F1116.140
C;Superfamily: Arabidopsis myb-related protein 1; myb DNA-binding repeat homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N;Alternate names: protein F1116.140
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 19-May-2000
                                                                                                                                                                                                           Gaps
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                                                                                                                                                  2; Length 393;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 55; DB 2; Length 399;
Pred. No. 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27.9%; Score 55; DB 2; Length 556; 42.3%; Pred. No. 64;
                                                                                                                                                                                                      10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                           MYB transcription factor-like protein - Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Experimental source: cultivar Columbia; BAC clone F1116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Cross-references: GB: M27815; NID: 9158000; PID: 9158001
                                                                                                                                                                         Pred. No. 47;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Mismatches
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                                                                                                                                            27.9%; Score 55; 45.5%; Pred. No. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C,Genetics:
A,Gene: FlyBase:numb
A,Cross-references: FlyBase:FBgn0002973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 QWLAARAGGCCGGGGIEGPTLRQWLA 33
A;Gene: CESP:C56A3.1
A;Map position: 5
A;Introns: 51/3; 91/1; 121/1: 331/3
                                                                                                                                                                                                                                                         4 PTLRQWLAARAGGGCGGGGIEG 25
                                                                                                                                                                                                                                                                                         76 PQVQPVYVQSGGGGGGGGGGG 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A:Residues: 1-399 <BEN>
A:Cross-references: EMBL:AL161667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27.9%;
55.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15 GGGGGGG-----IEGP 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41 GGGCGGGGGIRSKVKGP 58
                                                                                                                                                                                                   10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 55.6
Matches 10; Conservative
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                                                                                                                                                                         Similarity
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A;Molecule type: mRNA
A;Residues: 1-556 <UEM>
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Matches 11; Conserv
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                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                            Best Local
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                                                                                                                                                                                                Matches
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Gaps

14;

Gaps

13;

Indels

DB 2; Length 112;

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transcription factor Brn-2 - rat
NiAlternate names: class III POU domain protein brain-2
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 20-Feb-1998
C;Accession: A49447
R;Li, P; He, X; Gerrero, M.R.; Mok, M.; Aggarwal, A.; Rosenfeld, M.G.
Genes Dev. 7, 2483-2496, 1993
A;Title: Spacing and orientation of bipartite DNA-binding motifs as potential functio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rimevel-Ninio, M.; Terracol, R.; Kafatos, F.C.
EMBO J. 10, 2259-2266, 1991
A)Title: The ovo gene of Drosophila encodes a zinc finger protein required for female A; Reference number: $16356; MUID:91293102
A; Accession: $16356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule Lype: genomic RNA
A;Rosidues: 1-201 <ROT>
A;Cross-references: GB:D12477; GB:D01129; NID:g222674; PIDN:BAA02044.1; PID:d1002526;
A;Experimental source: Strain raspberry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical 20.2K protein - tomato ringspot virus
C;Species: tomato ringspot virus
C;Date: 31-Dec.1991 #sequence_revision 31-Dec-1991 #text_change 08-Oct-1999
C;Accession: JQ1094
                                                                                                                                                                                                                                                                                                                ovo protein - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 16-Feb-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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A;Reference number: JQ1093; MUID:91311402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27.7%; Score 54.5; DB 2; 57.9%; Pred. No. 1.4e+02;
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J. Gen. Virol. 72, 1505-1514, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13 RAGGGGGGGKEVFKAGRILLKVLKA 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Gene: FlyBase:ovo
A;Cross-references: FlyBase:FBgn0003028
A;Introns: 931/3; 1152/3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   434 AGSGGGCTGNGGGASGP 452
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                                     56
                                                                                                                71 AGSGGGGCTGNGGGGASGP 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-1213 <MEV>
A; Cross-references: EMBL:X59772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Status: translation not shown
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Matches 11; Conservative
                                     11 AARAGGGC---GGGGIEGP
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Best Local Similarity
Matches 15; Conserv
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                                                                                                                                                                                                                                         RESULT
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R;Garfinkel, M.D.; Wang, J.; Liang, Y.; Mahowald, A.P.
R;Garfinkel, M.D.; Wang, J.; Liang, Y.; Mahowald, A.P.
A;Title: Multiple products from the shavenbaby-ovo gene region of Drosophila melanogaste
A;Reference number: A56038; MUID:95021209
                         A.Title: Schistosome heat-shock proteins are immunologically distinct host-like antigens A.Reference number: A54507; MUID:88318804
A.Accession: A54507
A.Accession: A74507
A.Accession: A7
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A; Mesidues: 1-246 <ADDA.

A; Residues: 1-246 <ADDA.

A; Cross-references: EMBL: U44798; NID: 91174216; PIDN: AAA86654.1; PID: 91174217

A; Cross-references: EMBL: U44798; NID: 91174216; PIDN: AAA86654.1; PID: 91174217

C; Superfamily: unassigned ribonucleoprotein repeat homology <RRM>
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C;Species: Drosophila melanogaster
C;Date: 01-Dec-1995 #sequence_revision 01-Dec-1995 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Homo sapiens (man)
C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 05-Nov-1999
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A;Residues: 1-1028 <GAR>
A;Cross-references: GB:Ul1383; NID:9520526; PIDN:AAB60216.1; PID:9520527
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27.7%; Score 54.5; DB 2; Length 1028;
Best Local Similarity 57.9%; Pred. No. 1.2e+02;
Matches 11; Conservative 0; Mismatches 5; Indels 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 27.7%; Score 54.5; DB 2; Length 198; Best Local Similarity 41.4%; Pred. No. 29; Matches 12; Conservative 3; Mismatches 3; Indels 1.
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A,Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              168 RAGGGVPSGMPGGMPGAGGGGGKGPTIEE 196
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Biochem. Parasitol. 29, 275-282, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           U1-snRNP binding protein homolog - human
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Matches 12; Conservative
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R; Adams, D.
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A:Cross-references: GB:AL021646; GB:AL123456; NID:93242278; PIDN:CAA16640.1; PID:9282
A:Experimental source: strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            **Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blak Bult, C.J.; White, O.; White, O.; E.F.; Weinstock, K.G.; Morrick, J.M.; Glodek, rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A. Science 273, 1058-1073, 1996
**Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese A; Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannasc A; Rocession: F64408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Coenzyme F420 hydrogenase (EC 1.12.99.1) beta chain homolog - Methanococcus jannaschi N:Alternate names: coenzyme F420-reducing hydrogenase, beta subunit C;Species: Methanococcus jannaschii C;Species: Methanococcus jannaschii C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Superfamily: unassigned ferredoxin 2[4Fe-4S]-related proteins; ferredoxin 2[4Fe-4S]
C;Keywords: oxidoreductase
F;488-542/Domain: ferredoxin 2[4Fe-4S] homology <FER>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-620 < BUL>
A; Cross-references: GB: U67531; GB: L77117; NID: 92826342; PIDN: AAB98876.1; PID: 91591554
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C.Species: Drosophila melanogaster
C:Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000
C:Accession: T13807.
E:Goldstein, S.A.; Price, L.A.; Rosenthal, D.N.; Pausch, M.H.
Proc. Natl. Acad. Scl. U.S.A. 93, 13256-13261, 1996
A;Title: ORK1, a potassium-selective leak channel with two pore domains cloned from 1
A;Reference number: 217770; MUID:97075152
                                                                                                                                                                                                                                                                                                                       ó
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A; Residtes: 1-1001 <GOL>
A; Cross-references: EMBL:U55321; NID:g3808067; PID:g3808068; PIDN:AAC69250.1
                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                         27.4%; Score 54; DB 2; Length 495; 55.0%; Pred. No. 74; tive 0; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  potassium channel protein - fruit fly (Drosophila melanogaster)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27.4%; Score 54; DB 2; Length 620; 43.5%; Pred. No. 90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A:Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Mismatches
                                                                                                                 A;Gene: Rv3175
C;Superfamily: indoleacetamide hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Cross references: FlyBase: FBgn0017561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 EGPTLRQWLAARAGGGCGGGGIE 24
                                                                                                                                                                                                                                                                                                                                                                                                     147 GRTNNPWDAARTSGGSAGG 166
                                                                                                                                                                                                                                                                                                                                                                 3 GPTLRQWLAARAGGGGGGG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Map position: REV794850-792988
                                                                                                                                                                                                                                                                      Local Similarity 55.0%
hes 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C: Accession: F64408
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                                                                                                                                                                                                                                            Query Match
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                                                                                    C:Genetics:
                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42
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R.Molendijk, A.J.; Irvine, R.F.
R.Molendijk, A.J.; Irvine, R.F.
Plant Moll. Biol. 37, 53-56, 199
A.Title: Inositide signalling in Chlamydomonas: Characterization of a phosphatidylinosit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          probable amidase - Mycobacterium tuberculosis (strain H37RV)
C; Species: Mycobacterium tuberculosis
C; Species: Mycobacterium tuberculosis
C; Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C; Accession: E70948
R; Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A; Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A; Reference number: A70500; MUID: 98295987
A; Accession: E70948
                                                                                                                                                                                                                                      Superfamily: transcription factor Brn-1; homeobox homology; POU domain homology Keywords: DNA binding; homeobox; nucleus; transcription regulation
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A;Molecule type: DNA
A;Residues: 1-495 <COL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:U97663; NID:g2109290; PIDN:AAC50018.1; PID:g2109291
A;Experimental source: strain cw-15
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C.Species: Chlamydomonas reinhardtii
C.Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                       A;Status: preliminary; not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27.4%; Score 54; DB 1; Length 445; 60.0%; Pred. No. 68;
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                                                                                                                                                                  A; Experimental source: Derin
A; Note: sequence extracted from NCBI backbone (NCBIP:141696)
C; Superfamily: transcription factor Brn-1; homeobox homology;
C; Keywords: DNA binding; homeobox: nucleus; transcription reg
C; Keywords: DNA binding; homeobox: nucleus; transcription reg
F; 68-90/Region: glycine-rich
F; 153-165/Region: plutamine-rich
F; 133-165/Region: histidine/proline-rich
F; 133-165/Region: histidine/proline-rich
F; 271-338/Domain: POU domain homology <POU>
F; 357-413/Domain: homeobox homology <POU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Accession: T09084
A;Status: preliminary: translated from GB/EMBL/DDBJ
A;Residues: 1-490 <MOL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 231 GP----LIAAGGGGGGGGGSSPGDGSTARWDEWL 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 GPTLRQWLAARAGGGCGGGGI---EGPTLR--QWL 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A.Introns: 265/3; 331/3; 370/3; 455/1; 481/3
                                                                                 A; Molecule type: mRNA
A; Residues: 1-445 <LL1>
A; Cross-references: GB:L27663; NID:g443687
A; Reference number: A49447; MUID:94102531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best_Local Similarity 60.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8 OWLAARAGGGCGGG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 QWITALSHGGSGGG 74
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                             A; Accession: A49447
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27.4%; Score 54; DB 2; Length 1001;

Query Match

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Gaps ; 0

7; Indels

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A;Map position: 3
A;Introns: 17/3; 39/2; 146/3; 241/2
C;Superfamily: unassigned ribonucleoprotein repeat-containing proteins; ribonucleopro
                                                                                                                                                                                                                                                       A;Cross-references: EMBL:292826; PIDN:CAB07322.1; GSPDB:GN00021; CESP:C18D11.4 A;Experimental source: clone C18D11
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 17-Mar-2000 C;Accession: T19389  
R;Barlow, K. submitted to the EMBL Data Library, March 1997  
A;Reference number: Z19118  
A;Reference number: Z19118  
A;Accession: T19389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26.9%; Score 53; DB 2; Length 309; 52.6%; Pred. No. 63;
                                                                                                                                                                             A, Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 PILRQWLAARAGGGCGGG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 52.6%
Matches 10; Conservative
                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-309 <WIL>
                                                                                                                                                                                                                                                                                                                                                        A; Gene: CESP:C18D11.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Job time: 156 sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           qq
                                                                                                                                                                                                                                                                                                                                                                                                             R; Kawarabayasi, Y; Hino, Y; Horikawa, H; Yamazaki, S.; Haikawa, Y; Jin-no, K.; Takahawa, H; Takamiya, M; Masuda, S.; Funahashi, T; Tanaka, T.; Kudoh, Y; Yamazaki, J.; R DNA Res. 6, 83-101, 1999
A; Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr A; Reference number: A72771
A; Reference number: A72771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   probable U1 small nuclear ribonucleoprotein - fission yeast (Schizosaccharomyces pombe) C;Species: Schizosaccharomyces pombe C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000 C;Accession: T37948
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C;Superfamily: transformer-2 sex-determining protein; ribonucleoprotein repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-261 <SKE>
A; Residues: 1-261 <SKE>
A; Cross-references: EMBL:298974; PIDN:CAB11649.1; GSPDB:GN00066; SPDB:SPAC19A8.13
A; Experimental source: strain 972h-; cosmid c19A8
C; Genetics:
A; Gene: SPDB:SPAC19A8.13
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A;Experimental source: strain Kl
                                                                                                                                                                                                                                                                                                                                         C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
C;Accession: F72771
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R:Skelton, J.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V. submitted to the EMBL Data Library, September 1997
A; Reference number: 221756
A; Reference number: 27394
A; Accession: T3794
A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                         probable lysyl-tRNA Synthetase APE0161 - Aeropyrum pernix (strain K1)
                                                          ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27.2%; Score 53.5; DB 2; Length 562; 39.3%; Pred. No. 94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26.9%; Score 53; DB 2; Length 261; 50.0%; Pred. No. 55;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10; Indels
                                                             9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Genetics:
A;Gene: APB0161
C;Superfamily: Lyme disease spirochete lysine--tRNA ligase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein C18D11.4 - Caenorhabditis elegans C;Species: Caenorhabditis elegans
                             52.2%; Pred. No. 1.4e+02; ive 2; Mismatches 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           293 EWVSLRAGGREADMSSSGFTGITPREWL 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8 QWLAARAGG---GCGGGGIEGPTLRQWL 32
                                                                                                                                                      8 OWLAARAGGGGGGGGIEGPTLRQ 30
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Best Local Similarity 50.0%
Matches 9; Conservative
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Best Local Similarity 39.3%
Matches 11; Conservative
                                      Best Local Similarity 52.2
Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          T19389
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Dp
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

December 26, 2001, 10:27:54 ; Search time 10.22 Seconds (without alignments) 129.152 Million cell updates/sec Run on:

US-09-422-838C-33 197

1 IEGPTLROWLAARAGGGCGGGGIEGPTLROWLAARA 36 Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

100059 seqs, 36664827 residues Searched:

100059 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 00% Maximum Match 100% Listing first 100 summaries

SwissProt\_39:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

		Description	P34131 rattus norv		homod	chlan	_	_	8 ovis			_			P12795 schistosoma	_	L/O		_				064350 rattus nors						_	C	_		0		_
SUMMARIES	ď.	- 1	NT5_RAT	NT5_HUMAN	FXD2_HUMAN	SYA_CHLTR	HXD9_MOUSE	INS_BOVIN	INS_SHEEP	LAC1_NEUCR	LAC2_NEUCR	NUMB_DROME	SYA_CHLMU	LSR2_MYCTU	HS70_SCHJA	OVO_DROME	YR21_TRSVR	Y870_METJA	ORK1_DROME	SCO2_HUMAN	SYK_AERPE	GATA MYCLE	E2BE_RAT	SSB_RHOSH	SPIN_CBEPV	CYB_MICIK	RU17_DROME	PAC4_HUMAN	SIX3_MOUSE	FXD3_CHICK	HKLB_LYCES	OC3N_HUMAN	OC3N_MOUSE	SRF_XENLA	ERR1_MOUSE
	ad th	-:	209 1	210 1				105 1						112 1		1028 1	201 1						716 1				448 1			394 1			445 1		
dф	Query Match Length		32.2	30.7										27.7								26.9	26.9	26.6	26.6	26.6	26.6	26.6	26.4	26.4	26.4	26.4	26.4	26.4	26.4
	Score		63.5	60.5	09	28	57	56.5	56.5	26	26	52	52	54.5	54.5	54.5	54	54		53.5	ന	53		52.5	52.5	52.5	52.5	52.5	25	52	52	52	52	52	52
	Result No.		П	7	m	₹*	C)	9	7	ω .	σ,	10	11;	12	÷	14	15	16	17	18	19	20	21	22	233	24	25	97	27	58	23	30	31	32	33

053258 mycobacteri P20437 saccharomyc P12437 saccharomyc P1252 drosophila P1559 acanthamoeb P3681 neurospora P3557 sorghum bic 062376 mus musculu P08621 homo sapien 09837 gallus gall P20376 homo sapien P20376 homo sapien P27921 gallus gall P27921 gallus gall P37921 drosophila P37929 mus musculu P3770 cryptococuc P53783 mus musculu P37789 acropyrum p O94826 homo sapien P3778 mus musculu P37789 galcopyrum p O94826 homo sapien C41003 homo sapien C63959 mus musculu O9729 muscobacteri O90029 mesocricetu O95548 homo sapien P3531 isteria mo P50519 homo sapien P3512 ratus norv P35512 ratus norv P35513 lucilia cup Q07700 mycobacteri P44144 oryctolagus P36144 oryctolagus	P25545 xanthobacte P28356 hono sapien P08108 oncorbynchu Q25055 holotrichia P23813 mus musculu Q9jj54 rattus norv P51992 xenopus lae Q05925 homo sapien Q61169 mus musculu P56222 rattus norv Q03828 homo sapien P31361 mus musculu Q63262 rattus norv P20264 homo sapien P31361 mus musculu Q63282 rattus norv P31361 sestus norv P20264 homo sapien P31361 sestus perv P20264 homo sapien P31361 sestus norv P20264 homo sapien P31361 gastus perv P20264 homo sapien P36938 escherichia
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GATA_MYCTU CG11_YEAST CG11_YEAST CNG1_LEAST CNG1_LEAST CNG1_LEAST CNG1_LEAST CNG1_LEAST MYSC_ACACA MYSC_ACACACA MYSC_ACACACA MYSC_ACACACA MYSC_ACACACACACA MYSC_ACACACACACA MYSC_ACACACACACACA MYSC_ACACACACACACACACA MYSC_ACACACACACACACACACACACACACACACACACACA	CBBR XANFL HS70_CNCMT HS70_CNCMT HS70_CNCMT RASH_RRASH RRASH_RRASH RRASH
GATA_MYCTU GG12_YEAST GG11_YEAST GG11_YEAST GG11_YEAST GG11_YEAST GG11_YEAST KICJ_HUMAN MYSC_ACACA NYR_BORBI RU17_MOUSE RU17_MOUSE RU17_MOUSE RU17_MOUSE RU17_MOUSE RU17_MOUSE FXGA_CHICK MOUSE FYACA_MOUSE FYACA_MOUSE TYACA_MOUSE ONTO_HUMAN CIKK_MAT HUNA_MOUSE BET3_MESAU HUNA_RUSCU DDOI_MYCTU DPOI_MYCTU DPOI_MYCTU DYNA_CLIKE LSRC_MYCLE ERC_MYCLE ERC_MYCL	CGBRE_XANFL HXDS_HUMAN HXTO_CONCMT HOL3_HOLDI HACL3_HOLDI HXDB_MOUSE RXD_RAT HME1_HUMAN HME1_HUMAN HME1_HUMAN HME1_HUMAN GAT_ENT_ENT_ENT_ENT_ENT_ENT_ENT_ENT_ENT_EN
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ALIGNMENTS

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between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                         01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
NEUROTROPHIN-5 PRECURSOR (NT-5) (NEUROPHIC FACTOR 5) (NEUROTROPHIN-4)
                                                                                                                                                                                                                                             ID N.Y., Ibanez C.F., Nye S.H., McClain J., Jones P.F., Gies D.R., Belluscio L., le Beau M.M., Espinosa R. III, Squinto S.P., Persson H., Yancopoulos G.D.; and an eurotrophin-4: structure, chromosomal localization,
                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-92075279; Pubmed-1742028;
Berkemeter L.R., Winslow J.W., Kaplan D.R., Nikolics K., Goeddel D.V.,
                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                     'Neurotrophin-5: a novel neurotrophic factor that activates trk and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -1- FUNCTION: COULD SERVE AS A TARGET-DERIVED TROPHIC FACTOR FOR SENSORY AND SYMPATHETIC NEURONS.
-1- TISSUE SPECIFICITY: EXPRESSED IN TYMUS, MUSCLE, OVARY, BRAIN, HEART, STOMACH AND KIDNEY. EXPRESSED IN BOTH EMBRYO AND ADULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. . .) (POI
R -> P (IN REF 2)
W, DF5112COSC5D5B85 CRC64;
                                                                                                                                                                                                                                                                                                              tissue distribution, and receptor specificity.";
Proc. Natl. Acad. Sci. U.S.A. 89:3060-3064(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -i- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NEUROTROPHIN-5.
             209 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE-92212967; PubMed=1313578;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22332 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; S69323; AAB20548.1; -.
                                                                                                    (NT-4) (NEUTROPHIC FACTOR 4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00140; NGF; 1.
PROSITE; PS00248; NGF_1; 1.
PROSITE; PS50270; NGF_2; 1.
Growth factor; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP; P23560; 1BND.
InterPro; IPR002072; NGF.
Pfam; PF00243; NGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PD002052; NGF; 1.
             STANDARD;
                                                                                                                                          Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        169
198
200
75
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Neuron 7:857-866(1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00268; NGF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; JH0504; JH0504.
PIR; B42687; B42687.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     140
157
75
177
209 AA;
                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                     NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                         Rosenthal A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROPER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIGNAL
NT5_RAT
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Gaps

. 6

Indels

14;

2; Mismatches

Query Match 32.2%; Best Local Similarity 37.5%; Matches 15; Conservative

Score 63.5; DB 1; Length 209; Pred. No. 2.2;

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                                                                                                                            01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-FEB-1995 (Rel. 40, Last annotation update)
08-506-5001 (Rel. 40, Last annotation update)
NEUROTROPHIN-5 PRECURSOR (WT-5) (NEUTROPHIC FACTOR 5) (NEUTROPHIN-4)
(NT-4) (NEUTROPHIC FACTOR 4).
                                                                                                                                                                                                                                                                                                                  TISSUE=Prostate;
MEDLINE=92212967; PubMed=1313578;
MEDLINE=92212967; Nye S.H., McClain J., Jones P.F., Gies D.R.,
Ip N.Y., Ibanez C.F., Nye S.H., McClain J., Jones P.F., Gies D.R.,
Belluscio L., le Beau M.M., Espinosa R. III, Squinto S.P., Persson H.,
Yancopoulos G.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-92075279; PubMed-1742028;
Berkemeter L.R., Winslow J.W., Kaplan D.R., Nikolics K., Goeddel D.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Neurotrophin-5: a novel neurotrophic factor that activates trk and
                                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                     "Mammalian neurotrophin-4: structure, chromosomal localization,
                         128 GSPLRQYFFETRCKAESAGEGGPGVGGGGCRGVDRRHWLS 167
                                                                                                                                                                                                                                                                                                                                                                                                     tissue distribution, and receptor specificity.";
Proc. Natl. Acad. Sci. U.S.A. 89:3060-3064(1992)
3 GPTLRQWL------AARAGGGCGGGGIEGPTLRQWLA 33
                                                                                                      210 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  X-RAY CRYSTALLOGRAPHY (2.75 ANGSTROMS).
                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M86528; AAA60154.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00140; NGF; 1.
PROSITE; PS00248; NGF_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Interpro; IPR002072; NGF. Pfam; PF00243; NGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00268; NGF.
ProDom; PD002052; NGF; 1.
                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Neuron 7:857-866(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PDB; 188M; 09-FEB-99.
PDB; 1898; 26-FEB-99.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; JH0503; JH0503.
PIR; A42687; A42687.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                             NTF5 OR NTF4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MIM; 162662;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rosenthal A.
                                                                                                      NT5_HUMAN
                                                                         RESULT 2
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                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                      30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
FORKHEAD BOX PROTEIN D2 (FORKHEAD-RELATED PROTEIN FKHL17) (FORKHEAD-
RELATED TRANSCRIPTION FACTOR 9) (FREAC-9).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ernstsson S., Betz R., Lagercrantz S., Larsson C., Ericksson S., Cederberg A., Carlsson P., Enerbaeck S.; Cloning and characterization of freac-9 (FKHLL7), a novel kidney-expressed human forkhead gene that maps to chromosome 1p32-p34."; Genomics 46:78-85(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi,
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TAXID=9606;
                                                                                                                          N-LINKED (GLCNAC. . .) (POTENTIAL).
DBC6A30195E139AD CRC64;
                                                                                                                                                                                                                       6
                                                                                                                                                                                      30.7%; Score 60.5; DB 1; Length 210; 35.0%; Pred. No. 4.5;
                                                                                                                                                                                                                       14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (APR-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00657; FORK, HEAD 1; 1.
PROSITE; PS00658; FORK_HEAD_2; 1.
PROSITE; PS50039; FORK_HEAD_3; 1.
DNA-binding; Nuclear protein; Transcription regulation.
DOMAIN 101 104 POLY ALA.
                                                                                                                                                                                                                                                                     129 GSPLRQYFFETRCKADNAEEGGPGAGGGGCRGVDRRHWVS 168
                                                                                                                                                                                                                                                3 GPTLRQWL-----AARAGGGCGGGGIEGPTLRQWLA 33
                                                                  NEUROTROPHIN-5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -i- FUNCTION: PROBABLE TRANSCRIPTION FACTOR.
-i- SUBCELLULAR LOCATION: NUCLEAR.
-i- TISSUS SPECIFIC.
-i- SIMILARITY: CONTAINS I FORK-HEAD DOMAIN.
                                                                                                                                                                                                                                                                                                                                                             497 AA
                                                                                                                                                                                                                   3; Mismatches
                                   POTENTIAL.
PROSITE; PS50270; NGF_2; 1.
Growth factor; Signal; 3D-structure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=98066765; PubMed=9403061;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro: IPR001766; Fork_head.
Pfam; PF00250; Fork_head.
PRINTS; PR00053; FORKHEAD.
SMART; SM00339; FH; 1.
                                                                                                                                                                                                                                                                                                                                                                                       30-MAY-2000 (Rel. 39, Created)
                                                                                                                                       22426 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF042832; AAC15421.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                FOXD2 OR FKHL17 OR FREAC9.
                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                             80
210
170
199
                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                       210 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q63245; 2HFH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Enerbaeck S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                    30-MAY-2000
                                                                                                                                                                                                                                                                                                                                                          FXD2_HUMAN
060548;
                                                                        DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted
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                                                                                                                                     SEQUENCE
                                                                                                                        CARBOHYD
                                              PROPEP
                                SIGNAL
                                                             CHAIN
                                                                                                                                                                                                                 Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-99000809; PubMed-9784136;
Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind L.,
Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trachomatis.";
Science 282:754-759(1998).
-!- CATALYTIC ACTIVITY: ATP + L-ALANINE + TRNA(ALA) = AMP +
PYROPHOSPHATE + L-ALANYL-TRNA(ALA).
-!- SUBCELJULAR LOCATION: CYTOPLASMIC.
-!- SIMILARITY: BELONGS TO CLASS-II AMINOACYL-TRNA SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00980; TRNASYNTHALA.
PROSITE; PS00179; AA_TRNA_LIGASE_II_1; FALSE_NEG.
PROSITE; PS00339; AA_TRNA_LIGASE_II_2; 1.
Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14; Gaps
                                                                                                                                                                                                                                                                                                                                                 30-MAY-2000 (Rel. 39, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
ALANYL-TRNA SYNTHETASE (EC 6.1.1.7) (ALANINE--TRNA LIGASE) (ALARS).
                                                                                                                                                                          ;
                                                                                                                                        30.5%; Score 60; DB 1; Length 497; 66.7%; Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29.4%; Score 58; DB 1; Length 875;
                                                                                                                                                                         5; Indels
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                                                                                              EAAF498D216BE019 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                            Chlamydia trachomatis.
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
                                                                                                                                                                                                                                                                                                           875 AA.
                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 28;
            FORK-HEAD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AE001346; AAC68344.2; -.
InterPro; IPR002106; AA_tRNA_ligase_II.
InterPro; IPR003156; DHHA1.
                       POLY-ALA.
POLY-ALA.
                                                                 POLY-GLY.
POLY-ALA.
                                                      POLY-GLY
                                                                                                                                                                                                                                                                                                           PRT;
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217
250
306
306
426
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49007 MW;
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Pfam; PF01411; tRNA-synt_2c; 2.
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                                                                                                                                                                                                                              385 PTALLROGLKTDAGGGAGGGG 405
                                                                                                                                                                                                                                                                                                                                   30-MAY-2000 (Rel. 39, Created)
                                                                                                                                                                                                4 PT--LRQWLAARAGGGCGGG 22
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                                                                                                                                                                       Conservative
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Matches 15; Conservative
                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                           497 AA;
                                                                                                                                                   Similarity
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Best Local Sími
Matches 14;
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084754;
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                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-92224884; PubMed-1348690;
Renucci A.G.P., Zappavigna V., Zakany J., Izpisua-Belmonte J.-C.,
Buerki K., Douboule D.;
Comparison of mouse and human HOX-4 complexes defines conserved
sequences involved in the regulation of Hox-4.4.;
EMBO J. 11:1459-1468(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00027; HOMEOBOX_1: 1.
PROSITE; PS05001; HOMEOBOX_2: 1.
HOMEOBOX: DNA-binding; Developmental protein; Nuclear protein; Transcription regulation.
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  825 VQAHTLLAELLAPYGGRCGGKAISAQGSSAELPQIEFLNKTLRQWISTQ 873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       370DC47C6929F7E1 CRC64;
                                                                                                                                                                             01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
20-AuG-2001 (Rel. 40, Last annotation update)
HOMEOBOX PROTEIN HOX-D9 (HOX-4.4) (HOX-5.2).
HOXD9 OR HOXD-9 OR HOX-4.4)
                                                                                                                                  339 AA
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SER/THR-RICH.
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                                                                                                                                  PRT;
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InterPro; IPR001356; Homeobox.
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                                                                                                                                  STANDARD;
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$09569; $09569.
$20880; $20880.
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IRANSFAC; T01755; -
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                                                                                                                                HXD9_MOUSE
P28357;
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Gaps

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Conservative

Best Local Similarity Matches 13; Conserv

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Sanger F., Tuppy H.; "The amino-acid sequence in the phenylalanyl chain of insulin. 2. The investigation of peptides from enzymic hydrolysates."; Biochem. J. 49:481-490(1951).
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                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Salokangas A., Smyth D.G., Markussen J., Sundby F.; Bovine proinsulin: amino acid sequence of the C-peptide isolated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      х. кау CRYSTALLOGRAPHY.
Smith G.D., Duax W.L., Dodson E.J., Dodson G.G., de Graaf R.A.G.,
Reynolds C.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sanger F., Thompson B.O.P.;
"The amino-acid sequence in the glycyl chain of insulin. 2. The
investigation of peptides from enzymic hydrolysates.";
Biochem. J. 53:366-374(1953).
                                                                                                                                                                                                                                                                                                                                    MEDLINE=88288209; PubMed=2456452;
D'Agostino J., Younes M.A., White J.W., Besch P.K., Field J.B.,
                                                                                                                                                                                                                                                                                                                                                                                  "Cloning and nucleotide sequence analysis of complementary deoxyribonucleic acid for bovine preproinsulin."; Mol. Endocrinol. 1:327-331(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-71116409; PubMed-5545080;
Steiner D.F., Cho S., Oyer P.E., Terris S., Peterson J.D.,
Rubenstein A.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 25-54 AND 85-105, AND DISULFIDE BONDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=71166442; PubMed-4928892; Nolan C., Margoliash E., Peterson J.D., Steiner D.F.; "The structure of bovine proinsulin."; J. Biol. Chem. 246:2780-2795(1971).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The structure of des-Phe bl bovine insulin."; Acta Crystallogr. B 38:3028-3032(1982).
                                                                                                                                             21-JUL-1986 (Rel. 01, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ryle A.P., Sanger F., Smith L.F., Kitai R.; "The disulphide bonds of insulin."; Biochem. J. 60:541-556(1955).
                                                                                                              105 AA
                              101 GRYVRSWMEPLPGFPGGAGGGGGGGGGG 132
3 GPTLRQWL-----AARAGGGCGGGIEGP 26
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J. Biol. Chem. 246:1365-1374(1971).
                                                                                                              PRT;
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Eur. J. Biochem. 20:183-189(1971).
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                                                                                                                STANDARD;
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                                                                                                                                                                                                                               taurus (Bovine)
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                                                                                                                                                                                                INSULIN PRECURSOR.
                                                                                                                                                                                                                                                                                             NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                           Frazier M.L.;
                                                                                                              INS_BOVIN
P01317;
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                                                                                                 INS_BOVIN
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01-0CT-1996 (Rel. 34, Last sequence update) 01-0CT-1996 (Rel. 34, Last annotation update)
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                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                   Brange J., Dodson G.G., Edwards D.J., Holden P.H., Whittingham J.L., "A model of insulin fibrils derived from the X-ray crystal structure of a monomeric insulin (despentapeptide insulin)."; Proteins 27:507-516(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                   FUNCTION: INSULIN DECREASES BLOOD GLUCOSE CONCENTRATION. IT INCREASES CELL PERMEABILITY TO MONOSACCHARIDES, AMINO ACIDS AND FATTY ACIDS. IT ACCELERATES GLYCOLYSIS, THE PENTOSE PHOSPHATE CYCLE, AND GLYCOGEN SYNTHESIS IN LIVER.
SUBUNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO
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Insulin family; Hormone; Glucose metabolism; Signal; 3D-structure.
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                                                                                                                                                                                              SUBCELLULAR LOCATION: SECRETED. SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY. DATABASE: NAME-Protein Spotlight;
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INSULIN A CHAIN.
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Pfam; PF00049; Insulin; 1.
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MEDLINE=97285914; PubMed=9141131;
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A40909; A40909.
2INS; 31-MAY-84.
IAPH; 31-OCT-93.
IEPH; 31-OCT-93.
ICPH; 31-OCT-93.
ICPH; 31-OCT-93.
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Matches 13; Conserv
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PDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PDB;
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                                                                                                                                                                                                                                                                    Ohlsen S.M., Lugenbeel K.A., Wong E.A.; "Characterization of the linked ovine insulin and insulin-like growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peterson J.D., Nehrlich S., Oyer P.E., Steiner D.F., "Determination of the amino acid sequence of the monkey, sheep, and dog proinsulin C-peptides by a semi-micro Edman degradation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FIGURE 1. Chem. 247:4866-4871(1972).

-I' FUNCTION: INSULIN DECREASES BLOOD GLUCOSE CONCENTRATION. IT INCREASES CELL PERMEABILITY TO MONOSACCHARIDES, AMINO ACIDS AND FATTY ACIDS. IT ACCELERATES GLYCOLYSIS, THE PENTOSE PHOSPHATE CYCLE, AND GLYCOGEN SYNTHESIS IN LIVER.

-! SUBUNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO
                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: SECRETED.
SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000739; Insulin_IGF_relaxin.
Pfam; PF00049; Insulin; 1.
PRINTS; PR00276; INSULINA.
PRINTS; PR00277; INSULINB.
SMART; SM0078; IIGF; 1.
PROSITE; PS00262; INSULIN; 1.
Insulin family; Hormone; Glucose metabolism; Signal.
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Pred. No. 6.6;
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INSULIN A CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 25-54 AND 85-105.
Brown H., Sanger F., Kitai R.;
"The structure of pig and sheep insulins.";
Biochem. J. 60:556-565(1955).
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                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=94280618; PubMed=8011164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 IEGPTLRQWLAARAGGGGGGGGIEGP 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-72258016; PubMed-4626369;
                                                                                                                                                                                                                                                                                                                                                      DNA Cell Biol. 13:377-388(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U00659; AAB60625.1; -.
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50.0%;
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                                                                                                                                     Bovidae; Caprinae; Ovis.
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105
91
                                                     Cvis aries (Sheep).
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INSULIN PRECURSOR.
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HSSP; P01315; 9INS
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                                                                                                                                                           NCBI_TaxID=9940;
                                                                                                                                                                                                                                                                                                                             factor-II genes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 83:8854-8858(1986).
-!- FUNCTION: LIGNIN DEGRADATION AND DETOXIFICATION OF LIGNIN-DERIVED
PRODUCTS (PROBABLE).
-!- CATALYTIC ACTIVITY: 4 BENZENEDIOL + O(2) = 4 BENZOSEMIQUINONE +
                                                                                                                                                                                                                                         SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE-88087214; PubMed=2961749;
Germann U.A., Mueller G., Hunziker P.E., Lerch K.;
"Characterization of two allelic forms of Neurospora crassa laccase.
Amino- and carboxyl-terminal processing of a precursor.";
J. Blol. Chem. 263:885-896(1988).
                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 379-619 FROM N.A.
MEDLINE-87067412; PubMed=2947240;
Germann U.A., Lerch K.;
Isolation and partial nucleotide sequence of the laccase gene from Neurospora crassa: amino acid sequence homology of the protein to human ceruloplasmin.";
                                                               01-JUL-1989 (Rel. 11, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
LACCASE PRECURSOR (EC 1.10.3.2) (BENZENEDIOL:OXYGEN OXIDOREDUCTASE)
(URISHIOL OXIDASE) (LACCASE ALLELE OR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oxidoreductase; Signal; Copper; Metal-binding; Lignin degradation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -:- CONTACT: BINDS 4 CU-IONS PER MOLECULE. THREE DISTINCT CU CENTERS KNOWN AS TYPE 1 OR BLUE, TYPE 2 OR NORMAL, AND TYPE 3 OR COUPLED BINUCLEAR (BY SMILARITY).
-:- SUBCELLULAR LOCATION. SECRETED (POTENTIAL).
-:- SIMILARITY: BELONGS TO THE FAMILY OF MULTICOPPER OXIDASES.
-:- SIMILARITY: CONTAINS 3 PLASTOCYANIN-LIKE DOMAINS.
                                                                                                                                                          Neurospora crassa.
Eukaryota; Fungi; Ascomycota: Pezizomycotina; Sordariomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PLASTOCYANIN-LIKE 1.
PLASTOCYANIN-LIKE 2.
PLASTOCYANIN-LIKE 3.
COPPER (TYPE 2) (PROBABLE).
COPPER (TYPE 3) (PROBABLE).
COPPER (TYPE 3) (PROBABLE).
COPPER (TYPE 3) (PROBABLE).
COPPER (TYPE 1) (PROBABLE).
                619 AA
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PROSITE; PS00079; MULTICOPPER_OXIDASE1; 1.
PROSITE; PS00080; MULTICOPPER_OXIDASE2; 1.
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Interpro; IPR002355; MultiCu_oxidse2.
                                                                                                                                                                                      Sordariales; Sordariaceae; Neurospora.
NCBI_TaxID=5141;
                PRT;
                                                    01-JAN-1988 (Rel. 06, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL, M14554; AAA33590.1; -. EMBL; M18333; AAA33591.1; -. PIR: A28523; KSNCO. PIR; A29762; A29762.
                STANDARD;
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216
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              LAC1_NEUCR
P06811;
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LAC1_NEUCR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDILINE-8087214; PubMed=2961749; Germann U.A., Mueller G., Hunziker P.E., Lerch K.; Germann U.A., Mueller G., Hunziker P.E., Lerch K.; Characterization of two allelic forms of Neurospora crassa laccase. Amino- and carboxyl-terminal processing of a precursor."; Amino- and carboxyl-terminal processing of a precursor."; J. Biol. Chem. 263:885-896(1988).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-501-1989 (Rel. 11, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-FCB-1996 (Rel. 40, Last annotation update)
LACCASE PRECURSOR (C. 1.10.3.2) (BENZENEDIOL:OXYGEN OXIDOREDUCTASE)
(URISHIOL OXIDASE) (LACCASE ALLELE TS).
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-:- SUBCELLULAR LOCATION. SECRETED (POTENTIAL).
-:- SIMILARITY: BELONGS TO THE FAMILY OF MULTICOPPER OXIDASES.
-:- SIMILARITY: CONTAINS 3 PLASTOCYANIN-LIKE DOMAINS.
                                                                                                                                                                                                                     (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                          N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
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R (TYPE 2) (PROBABLE).
R (TYPE 3) (PROBABLE).
R (TYPE 1) (PROBABLE).
R (TYPE 1) (PROBABLE).
R (TYPE 1) (PROBABLE).
R (TYPE 1) (PROBABLE).
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                                                                                                                                                                                                                                                                                                                                                                FDED6D78B65048E3 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 56; DB
Pred. No. 34;
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InterPro; IPR001117; Cu-oxidase.
InterPro; IPR002355; MultiCu_oxidse2.
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COPPER
COPPER
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  COPPER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44 AERYGGG-GGGGCNSPINRQCW 64
                                                                                                                                                                                                                                                                                                                                                                      68198 MW;
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ilarity 63.6%;
Conservative
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Best Local Similarity
Matches 14; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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P10574;
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MEDLINE-99061335; PubMed-9846878;
Li S.-C., Zwahlen C., Vincent S.J., McGlade C.J., Kay L.E., Pawson T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster (Fruit fly).
Eukaryota: Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota: Neoptera: Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Structure of a Numb PTB domain-peptide complex suggests a basis for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE-89324081; PubMed=2752427;
Wemura T., Shepherd S., Ackerman L., Jan L.Y., Jan Y.N.;
"Numb, a gene required in determination of cell fate during sensory organ formation in Drosophila embryos.";
cell 58:349-360(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         diverse binding specificity.";

Nat. Struct. Biol. 5:1075-1083(1998).

-!- FUNCTION: NUMB IS REQUIRED IN DETERMINATION OF CELL FATE DURING SENSORY ORGAN FORMATION IN DROSOPHILA EMBRYOS. IT FUNCTIONS IN NUCLEI AND SEEMS TO INTERACT WITH NUCLEIC ACIDS.

-!- SUBCELLULAR LOCATION: NUCLEAR.

-!- SIMILARITY: CONTAINS 1 PID DOMAIN.
                                                                                                                                                                                                                                           N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                       (POTENTIAL).
                                                                                                                                                                                                                                                                                (POTENTIAL)
                                                                                                                                                                                                                                                                                               (POTENTIAL)
                                                                                                                                                                                                                                                                                                         (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                2;
                                                                                                                                                                                                                                                                                                                                                       Score 56; DB 1; Length 619;
Pred. No. 34;
                                                                                             COPPER (TYPE 2) (PROBABLE).
COPPER (TYPE 3) (PROBABLE).
COPPER (TYPE 3) (PROBABLE).
COPPER (TYPE 1) (PROBABLE).
COPPER (TYPE 2) (PROBABLE).
COPPER (TYPE 2) (PROBABLE).
COPPER (TYPE 3) (PROBABLE).
COPPER (TYPE 1) (PROBABLE).
COPPER (TYPE 1) (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                6; Indels
                                                                                                                                                                                                                                                                                                                     OBB6CCDE18841145 CRC64;
                                                                                                                                                                                                                                                                               N-LINKED (GLCNAC. . .)
N-LINKED (GLCNAC. . .)
                                                                                                                                                                                                                                                                   N-LINKED (GLCNAC. . .)
                                                            PLASTOCYANIN-LIKE 1.
PLASTOCYANIN-LIKE 2.
PLASTOCYANIN-LIKE 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                                                       N-LINKED (GLCNAC
                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                       LACCASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                     11 AARAGGCGGGGGIEGPTLRQ-W 31
                                                                                                                                                                                                                                                                                                                                                                                                                68120 MW:
                                                                                                                                                                                                                                                                                                                                                      28.48;
                                                                                                                                                                                                                                                                                                                                                     Query Match 28.4°
Best Local Similarity 63.6°
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
  Repeat.
                                                                                                                                                                                                                                                                                                                 619 AA;
                                                                                             Forman-Kay J.D.;
 Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMB PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMB_DROME
P16554;
                                                                                                                                                                                                                                           CARBOHYD
                                                                                                                                                                                                                                                       CARBOHYD
                                                                                                                                                                                                                                                                   CARBOHYD
                                                                                                                                                                                                                                                                               CARBOHYD
                                                                                                                                                                                                                                                                                          CARBOHYD
                                                                                                                                                                                                                                                                                                       CARBOHYD
                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                          DOMAIN
DOMAIN
DOMAIN
                      PROPEP
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METAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=MODN / NIGG;
MEDLINE=2015055; PubMed=10684935;
Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
Eisen J., Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
ALANYL-TRNA SYNTHETASE (EC 6.1.1.7) (ALANINE--TRNA LIGASE) (ALARS).
                                                                                                                                                                                                                                                  PROSITE; PS01179; PID; 1.
Nuclear protein; ATP-binding; Alternative initiation; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pņeumoniae AR39.";
                                                                                                                                                                                                                                                                                       NUMB PROTEIN, ZYGOTIC ISOFORM. NUMB PROTEIN, MATERNAL ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!" CATALYTIC ACTIVITY: ATP + L'ALANINE + TRNA(ALA) = AMP +
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 55; DB 1; Length 556;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                          4FECAAE9C98FEE71 CRC64;
                                                                                                                                                                                                                                                                                                                                      FOR MATERNAL ISOFORM.
ATP (POTENTIAL).
ARG/LYS-RICH (BASIC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chļamydia muridarum.
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              875 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 40;
4; Mismatches
                                                                                                                                                                                                                                                                                                                         (PROBABLE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic Acids Res. 28:1397-1406(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       486 OTLASGTGAAVGGGGPDDPFDAEWVA 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8 QWLAARAGGGGGGGGTEGPTLRQWLA 33
                                                                                                                                                                                                                                                                                                                                                                                            PID
                                                                                                                                                                                                     InterPro; IPR000050; PID_domain. Pfam; PF00640; PID; 1. SMART; SM00462; PTB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                      60628 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         27.9%;
                                                                                                                                    EMBL; M27815; AAA28730.1; -.
                                                                                                                                                                     PDB; 2NMB; 04-NOV-98.
FlyBase; FBgn0002973; numb.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 42.3:
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                       208
                                                                                                                                                                                                                                                                                                                                      42
22
25
81
81
556 AA;
                                                                                                                                                       A32466
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALAS OR TC0125
                                                                                                                                                       PIR; A32466;
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                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
SEQUENCE
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RESULT 14
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                                                                                                                                                                                                                                                                               1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=CDC 1551 / Oshkosh;
STRAIN=CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E., Rolconay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L., Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINGS S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamin N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quall M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Seelor K., Whitehead S., Barrell B.G.; Taylor K., Whitehead S., Barrell B.G.; Romplete genome sequence."; Mycobacterium tuberculosis from the Nature 393:537-544(1998).
                           InterPro; IPR001106; AA_tRNA_ligase_II.
InterPro; IPR0031156; DHHA1.
InterPro; IPR002318; tRNA-synt_2c.
Pfam; PF01411; tRNA-synt_2c; 1.
Pfam; PF02272; DHHA1; 1.
PRINTS; PR001990; TRNASYNTHAA.
PROSITE; PS00179; AA_TRNA_LIGASE_II_1; FALSE_NEG.
Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                               14;
                                                                                                                                                                                                                                                                                                                                 27.9%; Score 55; DB 1; Length 875; 28.6%; Pred. No. 58;
                                                                                                                                                                                                                                                                                                              1 IEGPTLRQWLAARAGGGGGGGGIE------GPTLRQWLAAR 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: DOMINNAT T-CELL ANTIGEN AND STIMULATES
LYMPHOPROLIFERATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                               5; Mismatches 16; Indels
                                                                                                                                                                                               98185 MW; A75F8977A23DC41D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
20-MG-2001 (Rel. 40, Last annotation update)
LSR2 PROTEIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 112 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LSR2 OR RV3597C OR MT3704 OR MTCY07H7B.25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-98295987; PubMed-9634230;
 EMBL; AE002279; AAF39003.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mycobacterium tuberculosis.
                                                                                                                                                                                                                                              Query Match
Best Local Similarity 28.6%
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                  Complete proteome. SEQUENCE 875 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-H37RV
                                                                                                                                                                                                                                                                                                                                                                                                                              LSR2_MYCTU
006285;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bishai W.;
                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 12
LSR2_MYCTU
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(7
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                                                                                                                                                                                                                                                                                                                                                         13; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schistosoma japonicum (Blood fluke).
Eukaryota; Metazoa: Platyhelminthes; Turbellarian Platyhelminths;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rhabditophora; Bulecithophora; Revertospermata; Mediofusata; Neodermata; Trematoda; Digenea; Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma. NCBI_TaxID=6182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hedstrom R., Culpepper J., Schinski V., Agabian N., Newport G., "Schistosome heat-shock proteins are immunologically distinct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOI. Blochem. Parasitol. 29:275-282(1988).
                                                                                                                                                                                                                                                                                            Query Match 27.7%; Score 54.5; DB 1; Length 112; Best Local Similarity 33.3%; Pred. No. 11; Matches 13; Conservative 6; Mismatches 7; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE 198 AA; 21845 MW; 800F8586046D5313 CRC64;
                                                                                                                                                                            CHAIN 19 112 LSR2 PROTEIN. SEQUENCE 112 AA; 12098 MW; A4B32E478CBAC3E4 CRC64;
                                                                                                               Antigen; Immune response; Signal; Complete proteome. SIGNAL 18
                                                                                                                                                                                                                                                                                                                                                                                                                      6 LRQWLAA-----RAGGGCGGGGI---EGPTLRQW 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   48 LKQWVAAGRRVGGRRRGRSGSGRGRGAIDREQSAAIREW 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-1989 (Rel. 12, Created)
01-OCT-1989 (Rel. 12, Last Sequence update)
01-UUL-1993 (Rel. 26, Last annotation update)
HEAT SHOCK 70 KDA PROTEIN (HSP70) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         198 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27.7%; Score 54.5; I
41.4%; Pred. No. 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP, P02593; 1CMF.
InterPro: IPR001023; HSP70.
PROSITE; PS00297; HSP70_1; PARTIAL.
PROSITE; PS00329; HSP70_2; PARTIAL.
PROSITE; PS01036; HSP70_3; PARTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE-88318804; PubMed-2457805;
                         EMBL; AE007170; AAK48061.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; M21011; AAA29897.1; -. PIR; A54507; A54507.
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EMBL; Z95557; CAB08947.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATP-binding; Heat shock.
                                                   TIGR; MT3704; -.
Tuberculist; Rv3597c; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               host-like antigens.";
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Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HS70_SCHJA
P12795;
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13 RAGG-----GCGGGGIEGPTLRQ 30

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             for female germ line development.";
EMBO J. 10:2259-2266(1991).
-!- FUNCTION: REQUIRED FOR SURVIVAL AND DIFFERENTIATION OF FEMALE GERM
                                                                                                                                                                                                                    Eukaryota: Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Garfinkel M.D., Wang J., Liang Y., Mahowald A.P.;
"Multiple products from the shavenbaby-ovo gene region of Drosophila melanogaster: relationship to genetic complexity.";
Mol. Cell. Biol. 14:6809-6818(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LINE CELLS. PLAYS A ROLE IN GERM LINE SEX DETERMINATION.
SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
DEVELOPMENTAL STAGE: FIRST APPEARS IN THE GERMARIUM AND
ACCUMULATES IN NIRES CELLS DURING OGGENESIS. STORED IN THE EGG,
BUT IS RAPIDLY LOST IN THE EMBRYOS EXCEPT FOR ITS CONTINUED
PRESENCE IN THE GERM LINE PRECURSOR POLE CELLS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mevel-Ninio M.T.M., Terracol R., Kafatos F.C., "The ovo gene of Drosophila encodes a zinc finger protein required
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART: SM00355; ZnF_C2H2; 4.
PROSITE; PS00028; ZINC_FINGER_C2H2_1; 3.
PROSITE; PS50157; ZINC_FINGER_C2H2_2; 3.
Zinc-finger; Metal-binding; DNA-binding; Repeat; Nuclear protein;
     OVO_DANGERS (STATE) (OVOIDER OF THE OFFICE O
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POLY-GLY.
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POLY-ASN.
POLY-GLN.
POLY-GLN.
POLY-GLN.
POLY-GLN.
POLY-GLN.
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                                                                                                                                                                                            Drosophila melanogaster (Fruit fly)
                                                                                                          20-AUG-2001 (Rel. 40, Last annotation OVO PROTEIN (SHAVEN BABY PROTEIN). OVO OR SVB.
                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Ovary;
MEDLINE=95021209; PubMed=7935398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=OREGON-R;
MEDLINE=91293102; PubMed=1712294;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U11383; AAB60216.1; -.
EMBL; X59772; CAB36921.1; ALT_SEQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Interpro; IPR000822; Znf-C2H2. Pfam; PF00096; zf-C2H2; 4. PRINTS; PR00048; ZINCFINGER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FlyBase; FBgn0003028; ovo.
  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  regulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP; P04002; 1WFA.
                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transcription
DROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
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                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                          Tomato ringspot virus (isolate raspberry) (Tomrsv).
Viruses; ssRNA posltive-strand viruses, no DNA stage; Comoviridae;
                                                                                                                                                                                                                   3,
                                                                                                                                                                                          DB 1; Length 1028;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27.4%; Score 54; DB 1; Length 201; 57.7%; Pred. No. 21;
                                                                                                                                                                                                                 Indels
                                                                                                                                           -> R (IN REF. 2).
D7068BBZBC0F6F77 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rott M.E., Tremaine J.H., Rochon D.M.; "Nucleotide sequence of tomato ringspot virus RNA-2."; J. Gen. Virol. 72:1505-1514(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POLY-GLY.
POLY-GLY.
9038506E18D7B450 CRC64;
                                                                                                                                                                                                                   2,
                                                                                                                                                                                                                                                                                                                                                      01-MAY-1992 (Rel. 22, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
HYPOTHETICAL 20.2 KDA PROTEIN IN RNA2.
                                                                                                                                                                                      27.7%; Score 54.5; D
57.9%; Pred. No. 75;
tive 0; Mismatches
                                                                                 ZINC FINGERS.
C2H2-TYPE.
                                                                                                                  C2H2-TYPE.
                                                                                                         C2H2-TYPE
                                                          POLY-GLN.
                        POLY-ALA
                                     POLY-ALA.
                                                POLY-GLN.
                                                                        POLY-GLN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE=91311402; PubMed=1856689;
                                                                                                                                                                                                                                                                                                                                          01-MAY-1992 (Rel. 22, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20194 MW;
                                                                                                                                                      110620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; D12477; BAA02044.1; -.
                                                                                                                                                                                                                                     11 AARAGGGC---GGGGIEGP 26
                                                                                                                                                                                                                                                            71 AGSGGGCTGNGGGGASGP 89
                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 57.7
hes 15; Conservative
                                                                                                                                                                                                                                                                                                                       STANDARD;
 5529
651
7258
802
8823
8932
992
992
                                                                                                                   953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22
66
148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; JQ1094; JQ1094.
HSSP; P04002; IWFA.
Hypothetical protein.
DOMAIN 15 2
                                                                                                                                                       AA;
                                                                                                                                                                                                  Local Similarity les 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       201 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=12281;
                                                                                                                                                                                                                                                                                                                      YR21_TRSVR
P25245;
                                                                                                                                                                                                                                                                                                                                                                                                                   Nepovirus
                                                                                                                              ZN_FING
CONFLICT
                                                                                                                                                                                       Query Match
                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                           ZN_FING
                                                                    DOMAIN
                                                                                                       ZNFING
                                                                                                                   ZNETNG
         DOMAIN
DOMAIN
                                  DOMAIN
                                             DOMAIN
                                                          DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                          YR21_TRSVR
                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                RESULT
q
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6; Indels 1; Mismatches 13 RAGGGGGGGIE----GPTLRQWLAA 34 13 RAGGGGGGKEVFKAGRTLLKVLKA 38 Matches q

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Gaps

4,

RESULT 16 7870\_METJA

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                                                                                                                                                                            MEDLINE-96337999; PubMed-8688087;
Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D., Morte O., Olsen G.J., Zhou L., Fleischmann R.D., Gocayne J.D., Sulton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D., Sulton G.G., Blake J.A., Tomb J.-F., Adams M.D., Reich C.I., Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A., Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nuyyen D., Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C., Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M., Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C., "Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                   Science 273:1058-1073(1996).
--- SIMILARITY: TO COENZYME F420 HYDROGENASE BETA SUBUNIT.
--- SIMILARITY: TO M.JANNASCHII MJ1349, MJ0725 AND MJ0551.
--- SIMILARITY: THE C-TERNINAL DOMAIN IS A 4FE-4S/SIROHEME DOMAIN FOUND IN NITRITE REDUCTASES (EC 1.6.6.4 AND EC 1.7.7.1) AND SULFITE REDUCTASES (EC 1.8.1.2 AND EC 1.8.7.1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein; Oxidoreductase; Heme; Iron-sulfur; 4Fe-4S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IRON-SULFUR (4FE-4S) (POTENTIAL).
IRON-SULFUR (4FE-4S) (POTENTIAL).
IRON-SULFUR (4FE-4S) (POTENTIAL).
IRON-SULFUR (4FE-4S) AND SIROHEME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 620;
                                                                                                    Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (BY SIMILARITY).
9D71D2580D7D0BA8 CRC64;
                          (Rel. 35, Created)
(Rel. 35, Last sequence update)
(Rel. 40, Last annotation update)
  620 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27.4%; Score 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF01077; NIR_SIR; 1.
PRINTS; PR00397; SIRODAEM.
PROSITE; PS00198; 4FE4S_FERREDOXIN; 2.
PROSITE; PS00365; NIR_SIR; 1.
                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-JAL-1 / DSM 2661 / ATCC 43067;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Interpro; IPR001450; 4FE4S_ferrdxin.
Interpro; IPR000660; Nir_Sir.
  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             620 AA; 69793 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U67531; AAB98876.1; -.
                                                    20-AUG-2001 (Rel. 40, Last a HYPOTHETICAL PROTEIN MJ0870.
                                                                                         Methanococcus jannaschii.
     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00037; fer4; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q45560; 1BQX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Complete proteome.
                                                                                                                             NCBI_TaxID=2190;
                                                                                                                     Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MJ0870
                                      01-NOV-1997
                            01-NOV-1997
                                                                                                                                                                                                                                                                                                             jannaschii.
     Y870_METJA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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Adams M.D. Celniker S.E. 11 P.W. Hoskins R.A., Gocayne J.D.,
RA Adams M.D. Celniker S.E. 11 P.W. Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E. 11 P.W. Hoskins R.A., Galle R.F.,
RA George R.A. Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Bardon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfelifer B.D.,
RA Bardon R.C., Rogers Y.-H.C., Halt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews Pfennkoch C., Baldwin D.,
Ballew R.M., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Beeson K.Y., Benos P.V., Deng Z., Mays A.D., Deviller P., Sottler P., Chandra I.,
Ra Cherry J.M. Cawles P., Deng Z., Mays A.D., Devilles P., Dunn P.,
RA Cherry J.M., Cawles S., Delchor A., Deng Z., Mays A.D., Dew I., Ditez S.M.,
A cherry J., Evangelista C.C., Ferrac C., Serrices S., Pleischman W.,
RA Dodson K., Doup L.E., Downes M., Dung Z., Guan P., Houck J.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Marvey D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Leviteky A.A., Li J., Wei M.-Y., Mcched M.P., Mccheler R.,
A Jalail M., Mattel B., McIncosh T.C., Morris J., Mosherson D.,
RA Mount S.M. Moy M. Murphy B., Murphy L., Muzny D.M., Natheria A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Mosherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Mosherson D.,
RA Melson D.R., Nelson K.A., Nixon K., Nussken D. P., Scheler F., Shen H.,
RA Melson D.R., Nelson K.A., Nixon K., Nuskern D.K., Peeleber F., Shen H.,
RA Meng C. Stending A.C., Stapleton M., Stupsk M. P., Xang S., Yao Q.A.,
RA Meng C.F., Zaveri J.S., Zhan M., Zhong W., Zhu S., Zhu X., Shill H.O.,
RA Meng C.F., Zaveri J.S., Zhan M., Zhong W., Zhu S., Zhu X., Shill H.O.,
RA Meng C.F., Zaveri J.S., Zave
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -1- TISSUE SPECIFICITY: WIDESPREAD EXPRESSION IN ADULT, STRONGEST EXPRESSION IN MUSCLE, BRAIN AND OVARY. ALSO PRESENT AT LOW LEVELS
20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
OPEN RECTIFIER POTASSIUM CHANNEL PROTEIN 1 (TWO PORE DOMAIN POTASSIUM
                                                                                                                                                                                             Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -i- MISCELLANEOUS: INHIBITED BY BARIUM.
-i- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Goldstein S.A.N., Price L.A., Rosenthal D.N., Pausch M.H., "ORKI, a potassium-selective leak channel with two pore domains cloned from Drosophila melanogaster by expression in Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -1. SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Proc. Natl. Acad. Sci. U.S.A. 93:13256-13261(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=20196006; Pubmed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=97075152; PubMed=8917578;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LARVA AND EMBRYO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IS REVERSED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-BERKELEY;
                                                                                                                                                                       ORK1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHANNELS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cerevisiae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Larva
                                                                                                                                                                       CHANNEL
```

; 0

Gaps

; 0

10; Indels

Mismatches

> g ò

Pred. No. 55;

43.5%;

Conservative

PRT; 1001 AA.

STANDARD;

ORK1\_DROME Q94526;

RESULT 17 ORK1\_DROME

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ·;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-20014747; PubMed=10545952;
Papadopoulou L.C., Sue C.M., Davidson M.M., Tanji K., Nishino I.,
Sadlock J.E., Krishna S., Walker W., Selby J., Glerum D.M.,
Van Coster R., Lyon G., Scalais E., Lebel R., Kaplan P., Shanske S.,
De Vivo D.C., Bonilla E., Hirano M., DiMauro S., Schon E.A.;
"Fatal infantile cardioencephalomyopathy with COX deficiency and
mutations in SCQ2, a COX assembly gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- FUNCTION: THOUGHT TO PLAY A ROLE IN EITHER MITOCHONDRIAL COPPER TRANSPORT OR INSERTION OF COPPER INTO THE ACTIVE SITE OF COX.
-!- SUBCELLULAR LOCATION: MITOCHONDRIAL (BY SIMILARITY).
                                                                                                                                                                                                                                                          Ionic channel; Transmembrane; Ion transport; Potassium transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                     N-LINKED (GLCNAC. .) (POTENTIAL).

M; 09AE1A3669072E07 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 54; DB 1; Length 1001;
Pred. No. 83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A., AND VARIANTS FIC LYS-140 AND PHE-225.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Smink L.J., Burton J.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                   PORE-FORMING (POTENTIAL). POTENTIAL.
                                                                                                                                                                                                                                                                                                                       PORE-FORMING (POTENTIAL).
                                                                                                                                                                                                                                                                                              CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                         CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                    CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  266 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
                                                                                                                                                                                                                                                                                                              POTENTIAL.
                                                                                                                                                                                                                                                                                                                                           POTENTIAL
                                                                                                                                   EMBL, U55321; AAC69250.1; -- EMBL, AE003484; AAF47972.1; -- FlyBase; FBgn0017561; Orkl. InterPro; IPR003280; Zporek_channel. InterPro; IPR001622; Channel_pore_K. InterPro; IPR001699; TWIK_channel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     761 QQQAAAGGAAGGGGISRGSRKQ 783
                                                                                                                                                                                                                            Pfam; PF02034; TWIK_channel; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 109289 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8 QWLAARAGGGCGGGGIEGPTLRQ 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SCO2 PROTEIN HOMOLOG PRECURSOR.
                                                                                                                                                                                                                                             PRINTS; PR01333; 2POREKCHANEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-MAY 2000 (Rel. 39, Created)
30-MAY 2000 (Rel. 39, Last seq
20-AUG-2001 (Rel. 40, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27.483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                       111
140
170
191
224
264
1001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                              1001 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Monocytes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                    171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SCO2_HUMAN (043819; Q9UK87;
                                                                                                                                                                                                                                                                            Glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12;
                                                                                                                                                                                                                                                                                                                                                       DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                         TRANSMEM
                                                                                                                                                                                                                                                                                                                                      FRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                    PRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                   CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SCO2_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ωp
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-!- TISSUE SPECIFICITY: UBUIQUITOUS.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'n
DISEASE: DEFECTS IN SCO2 ARE THE CAUSE OF FATAL INFANTILE
CARDIOENCEPHALOMYOPATHY WITH COX DEFICIENCY. THIS DISEASE IS
CHARACTERIZED BY HYPERTROPHIC CARDIOMYOPATHY, LACTIC ACIDOSIS, AND
GLIOSTS. HEART AND SKELFTAL MUSCLE SHOW REDUCTIONS IN COX
ACTIVITY, WHEREAS LIVER AND FIBROBLASTS SHOW MILD COX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kawarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y., Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S., Naqai Y., Nishijima K., Nakazawa H., Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K., Nakamura Y., Nomura N., Sako Y., Kikuchi H., Complete genome sequence of an aerobic hyper-thermophilic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PYROPHOSPHATE + L-LYSYL-TRUA(LYS).
--- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
--- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
LYSYL-TRNA SYNTHETASE (EC 6.1.1.6) (LYSINE--TRNA LIGASE) (LYSRS).
LYSS OR APE0161.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Archaea; Crenarchaeota; Desulfurococcales; Desulfurococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 266;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cremarchaeon, Aeropyrum pernix Kl.";
DNA Res. 6:83-101(1999).
-!- CATALYTIC ACTIVITY: ATP + L-LYSINE + TRNA(LYS) = AMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 LRQWLAARAGGG--CGGGGIEGPTLR-------QWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33 LRSWLLSRQGPAETGGQGQPQGPGLRTRLLITGLFGAGLGGAWLALRA 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                         E -> K (IN FIC).
/FTId=VAR_008874.
S -> F (IN FIC).
/FTId=VAR_008875.
R -> P (IN REF. 1).
W; BC2F40E057329BF3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                            MITOCHONDRION (POTENTIAL). SCO2 PROTEIN HOMOLOG.
                                                                                                                                                                                                                                                                                                                                                             Interpro; IPR003782; SCOl_SenC.
Pfam; PF02630; SCOl-SenC; 1.
Mitochondrion; Transit peptide; Disease mutation.
                                                                                                        SIMILARITY: BELONGS TO THE SCO1/2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 562 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 30;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27.2%; Score 53.5; 35.4%; Pred. No. 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=99310339; PubMed=10382966;
                                                                                                                                                                                                                                                                               EMBL; AF177385; AAF05313.1; -. EMBL; AL021683; CAA16671.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29810 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 35.49
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               225
                                                                                                                                                                                                                                                                                                                                                                                                                                          266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 266 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                      DEFICIENCIES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Aeropyrum.
NCBI_TaxID=56636;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Aeropyrum pernix
                                                                                                                                                                                                                                                                                                                                                                                                                                                             140
                                                                                                                                                                                                                                                                                                                MIM; 604272; -.
                                                                                                                                                                                                                                                                                                                                      604377;
                                                                                                                                                                                                                                                                                                                                                      MIM; 220110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SYK_AERPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=K1
                                                                                                                                                                                                                                                                                                                                                                                                                          TRANSIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                             VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9YFT9;
                                                                                                                                                                                                                                                                                                                                                                                                                                            CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SYK_AERPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
 δλ
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Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R.,
Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,
Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,
Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,
Murphy L., Oliver K., Quail M.A., Rajandream M.-A., Rutherford K.M.,
Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
                                                                                                                                                                                                             Pfam; PF01921; tRNA-synt_1f; 1.
PROSITE; PS00178; AA_TRNA_LIGASE_1; FALSE_NEG.
Aminoacy1-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mycobacterium leprae.
Bacteria; Firmloutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1769;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
20-MUG-2001 (Rel. 40, Last annotation update)
GLUTAMYL-TRNA(GLN) AMIDOTRANSFERASE SUBUNIT A (EC 6.3.5.-) (GLU-ADT
                                                                                                                                                                                                                                                                                                                                                                                                               3;
                                                                                                                                                                                                                                                                                                                                                                     27.2%; Score 53.5; DB 1; Length 562; 39.3%; Pred. No. 58; tive 4; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                   "KMSKS" REGION.
753664E2937FBF27 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Massive gene decay in the leprosy bacillus.";
Nature 409:1007-1011(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             497 AA.
                                                                                                                                                                                                                                                                                  "HIGH" REGION.
                                                                                                                                                                       InterPro; IPR001412; tRNA-synt_I.
InterPro; IPR002904; tRNA-synt_lys_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    293 EWVSLRAGGREADMSSSGFTGITPREWL 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                8 QWLAARAGG---GCGGGGGIEGPTLRQWL 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                  50 58 "
305 309 "
562 AA; 65114 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GATA OR ML1702 OR MLCB637.13.
                                                                                                                                                            EMBL: AP000058; BAA79072.1;
                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 39.3%
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                       Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GATA_MYCLE
033105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBUNIT A)
                                                                                                                                                                                                                                                                                                                          SEQUENCE
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q
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and for commercial
         entities requires a license agreement (See http://www.isb-sib.ch/announce.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biochim, Biophys. Acta 1307:318-324(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SIMILARITY: BELONGS TO THE EIF-2B GAMMA/EPSILON SUBUNITS FAMILY.
                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
TRANSLATION INITIATION FACTOR EIF-2B EPSILON SUBUNIT (EIF-2B GDP-GTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -:- SUBUNIT: COMPLEX OF FIVE DIFFERENT SUBUNITS; ALPHA, BETA, GAMMA, DELTA AND EPSILON.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=SPRAGUE-DAWLEY;
MEDILINE=96305355; PubMed=8688467;
Flowers K.M., Mellor H., Matts R.L., Kimball S.R., Jefferson L.S.;
Flowers K.M., Mellor H., Matts R.L., Kimball S.R., Jefferson L.S.;
"Cloning and characterization of complementary and genomic DNAs
encoding the epsilon-subunit of rat translation initiation
                                                                                                                                                                                                                                                                                .;
0
                                                                                                                                                                                                                                         26.9%; Score 53; DB 1; Length 497; 52.6%; Pred. No. 59;
                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C6E4BFCE060AF6F1 CRC64;
Usage by
                                                                                                                                                                          Protein biosynthesis; Ligase; Complete proteome.
SEQUENCE 497 AA; 51536 MW; D3723D871518BDC7 CRC64;
                                                                                                                                                                                                                                                                                 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Amino-acid biosynthesis; Translation regulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                           716 AA.
modified and this statement is not removed.
                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POLY-GLY.
POLY-PRO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Interpro; IPR001451; Hexapep_transf.
Interpro; IPR003307; eIF5C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1997 (Rel. 35, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80240 MW;
                                                                                                                                       Pfam; PF01425; Amidase; 1.
PROSITE; PS00571; AMIDASES; 1.
                                                                                   AL583923; CAC30655.1; -.
                                                                                                                      InterPro; IPR000120; Amidase.
                                                                    EMBL; 299263; CAB16428.1; -.
                                                                                                                                                                                                                                                                                                                                                      145 GPTRNPWNVDRVPGGSGGG 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U19516; AAB17690.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U19511; AAB17691.1; -
                                                                                                                                                                                                                                                                                                                     3 GPTLRQWLAARAGGGCGGG 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00132; hexapep; 3. Pfam; PF02020; W2; 1. SMART; SM00515; eIF5C; 1.
                                                                                                                                                                                                                                                                 Local Similarity 52.6 nes 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2-BOUND GDP FOR GTP.
                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             716 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EXCHANGE FACTOR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10116;
                                                                                                         Leproma; ML1702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EIF2B5 OR EIF2BE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   factor-2B.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                             E2BE_RAT
064350;
                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 21
                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                              E2BE_RAT
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                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIR-ATCC (17023 / 2.4.1 / NCIB 8253 / DSM 158;
STRAIR-ATCC (17023 / 2.4.1 / Kaplan S.;
Zeilstra-Fyalls J.H., Kaplan S.;
Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION. THIS PROTEIN IS ESSENTIAL FOR REPLICATION OF THE CHROMOSOME. IT IS ALSO INVOLVED IN DNA RECOMBINATION AND REPAIR (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P50 OR SPH.
Choristoneura biennis entomopoxvirus (CbEPV).
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Entomopoxvirinae;
                                                                                                                                                                                                                                              30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
SINGLE-STRAND BINDING PROTEIN (SSB) (HELIX-DESTABILIZING PROTEIN).
                                                                                                                                                                                                                                                                                                                Rhodobacter sphaeroides (Rhodopseudomonas sphaeroides).
Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group;
                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 174;
   DB 1; Length 716;
                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA replication, MW; DBF5BC8D034D532D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                            174 AA.
                                  3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 52.5; I
Pred. No. 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: BELONGS TO THE SSB FAMILY.
   Score 53;
                                                                  11 AARAGGGGGGGIEG-----PTLRQWLAA 34
                                                                                                    15 ANKRGGGSGGGTQGAEEPPPPLQAVLVA 44
                    Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP, P02339; IKAW.
INTERPO: IPR000424; SSB.
PFam: PF00436; SSB. 1.
PROSITE; PS00735; SSB_1; FALSE_NEG.
PROSITE; PS00736; SSB_2; FALSE_NEG.
                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPINDOLIN PRECURSOR (SPHEROIDIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .;
0
                                                                                                                                                                                                                        30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last seq
30-MAY-2000 (Rel. 39, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA-binding; DNA repair; DNA resource 174 AA; 18496 MW;
26.9%;
43.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U82280; AAD00529.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | |||| |||| |
| 122 AGAGGMGGGGYEDRGGP 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12 ARAGGGCGGGGIE---GP 26
                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12; Conservative
                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Entomopoxvirus B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10288;
                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=1063;
                                                                                                                                                                                                                                                                                                                                                   Rhodobacter
                                                                                                                                                                                         SSB_RHOSH
Q92AQ8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPIN_CBEPV
Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                  Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 23
SPIN_CBBEW
ID SPIN_C
AC P23061
DT 01-NOW
DT 20-NOG
DE SPINDO
GN PSO ON
CO VITUSE
OC VITUSE
OC BETCOMC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                 Matches
                                                                                                                                                                      SSB_RHOSH
                                                                                                                                                        RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mtDNA sequences.";
Mol. Phylogenet. Evol. 15:157-164(2000).
''- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE
COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A
RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL
COUPLED TO ATP SYNTHESIS (BY SIMILARITY).
'-- COFACTOR: TWO HEME GROUPS (ES52 AND B566) WHICH ARE NOT COVALENTLY
BOUND TO THE PROTEIN (BY SIMILARITY).
-- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,
                                                                                                                                                                                                                                                          MEDLINE-93389435; PubMed-8376960;
Dall D., Sriskantha A., Vera A., Lai-Fook J., Symonds T.;
"A gene encoding a highly expressed spindle body protein of Heliothis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Elapidae; Notechinae; Micropechis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Slowinski J.B., Keogh J.S.; "Phylogenetic relationships of elapid snakes based on cytochrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- CAUTION: WAS ORIGINALLY (REF.1) THOUGHT TO BE A SPHEROIDIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ٠.
ش
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: WITH HAEPV SPINDOLIN AND ACMNPV SPINDOLIN-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 341;
                                                             Yuen L., Dionne J., Arif B., Richardson C.; "Identification and sequencing of the spheroidin gene of Choristoneura biennis entomopoxvirus."; Virology 175:427-433(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E84EF9BCD901E72F CRC64;
                                                                                                                                                                                                                                                                                                                                                         armigera entomopoxvirus.";
J.:Gen. Virol. 74:1811-1818(1993).
-I- FUNCTION: THIS PROTEIN IS A SINDLE BODY PROTEIN.
-I: SUBUNIT: HOMODIMER; DISULFIDE-LINKED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26.6%; Score 52.5; DB 1; 44.8%; Pred. No. 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Rel. 40, Last sequence update) (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  370 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Mismatches
SEQUENCE FROM N.A., AND SEQUENCE OF 21-50.
MEDLINE=90223988; Pubmed=2327073;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPINDOLIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 PTLROWLAARAGGG----CGGGGIEGPTLR 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. MEDLINE=20229584; PubMed=10764543;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-AUG-2001 (Rel. 40, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38709 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M34140; AAA42887.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; A34743; PYVZCB.
Signal; Late protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MTCYB OR COB OR CYTB.
                                                                                                                                                                                                                         REVISION TO FUNCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Micropechis ikaheka.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE 341 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=66188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CYTOCHROME B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9MLK2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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TD CYB_M

DT 20-AU

DT 20-AU

DT 20-AU

DT 20-AU

DE CYTOC

GN MICCYB

OC ELBPL

OC ELBPL

OX MICCYB

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RESULT 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mack by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MeDLINE-20196006; PubMed-10731132;
Adams W.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adams W.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
Adams W.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
A Sutton G.G., Wortman J. R., Yandell M.D., Zhang O., Chan L. X.,
Bandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfelifer B.D.,
Wan K. H., Doyle C., Baxeer E.G., Halt G., Nalson C.R., Mikkos G.L.G.,
Abril J.F., Apbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davles P.,
A de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 25
RU17_DROME STANDARD; PRT; 448 AA.
AC P17133; Q9VM56; DT 01-AuG-1990 (Rel. 15, Created)
DT 20-AuG-2001 (Rel. 40, Last sequence update)
DT 20-AuG-2001 (Rel. 40, Last sequence update)
DF 20-AuG-2001 (Rel. 41, Last sequence update)
DF 20-AuG-2001 (Rel. 40, Last sequence update)
DF 20-AuG-2001 (Rel. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE-90258833; Pubmed-1692955;
Mancebo R., Lo P.C.H., Mount S.M.;
"Structure and expression of the Drosophila melanogaster gene for the Ul small nuclear ribonucleoprotein particle 70K protein.";
Mol. Cell. Biol. 10:2492-2502(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pterygota: Neoptera: Endopterygota: Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                     EMBL; AF217826; AAF37245.1; -.
InterPro; IPR000179; Cyt_b_b6.
Pfam; PF00032; cytochrome_b_c; 1.
Pfam; PF00033; cytochrome_b_c; 1.
PROSTTE; PS00193; CYTOCHROME_B, OO; 1.
PROSTTE; PS00192; CYTOCHROME_B_HEME; FALSE_NEG.
Electron transport; Mitochondrion; Respiratory chain; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 75 75 IRON 1 (HEME B562 AXIAL LIGAND).
89 89 IRON 2 (HEME B566 AXIAL LIGAND).
174 174 IRON 2 (HEME B562 AXIAL LIGAND).
188 IRON 1 (HEME B566 AXIAL LIGAND).
370 AA; 42083 MW; CCDE45269CAB2B9D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26.6%; Score 52.5; DB 1; Length 370; 41.9%; Pred. No. 51;
CYTOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY). SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         149 GPTLTTWL------WGGFSINDPTLTRFFA 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 GPTLRQWLAARAGGGCGGGGIEGPTLRQWLA 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 41.9°
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-Berkeley;
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Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

Burbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann M.,

Rosler C., Gabriellan A.E., Garg N.S., Gelbart W.M., Glasser K.,

Glodek A., Gong F., Gorrell J.H., G. 2., Guan P., Harris M.,

Harris N.L., Harvey D., Heinan T.J., Hernandez J.R., Houck J.,

RA Harris N.L., Harvey D., Howland T.J., Wei M.-H., Ibegwam C.,

A Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Mattei B.L., McIntosh T.C., McLeod M.P., Moshrefi A.,

Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Reinert K., Remington K.B., Nixon K., Subsken D.R., Pacleb J.M.,

Shue B.C., Siden Kiamos I., Simpson M., Skupski M.P., Smith T.,

Shue B.C., Siden Kiamos I., Simpson M., Skupski M.P., Smith T.,

RA Syirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

RA Well J., Wassarman D.A., Weinstock G.M., Weissenbach J.,

RA Syirskas R., Tector C., Turner R., Venter E., Wang S., Yao Q.A.,

RA Shirskas R., Woodege T., Worley K.C., Wu D., Yang S., Yao Q.A.,

RA Shong X.H., Zhong F.W., Rubin G.M., Venter J.C.;

RA Glibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;

Ra Glibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;

FRU FUNCTION: MEDIATES THE SPLICING OF PRE-MRNA BY BINDING TO THE STEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PAC4_HUMAN STANDARD; PRT; 969 AA.
P29122; 015099; 015100; 09UEJ1; 09UEJ2; 09UEJ7; 09UEJ8; Q9UEJ9; 09Y4G9; 005509; 005100; 09VH1; 01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
01-DEC-1992 (Rel. 40, Last annotation update)
PALRED BASIC AMINO LECATING ENZYME 4 PRECURSOR (EC 3.4.21.-)
(SUBTILISIN/KEXIN-LIKE PROTEASE PACE4) (SUBTILISIN-LIKE PROPROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PEGNIS, FRM, 1.
SMART: SM00360; RRM; 1.
PROSITE: PS501020; RRM; 1.
PROSITE: PS0003030; RRM, RNP_1; 1.
Nuclear protein; Ribonucleoprotein; RNA-binding; mRNA processing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RNA-BINDING (RRM).
ARG/GLU-RICH (MIXED CHARGE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SIMILARITY: CONTAINS 1 RNA RECOGNITION MOTIF (RRM).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N -> S (IN REF. 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
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InterPro; IPR000504; RRM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AE003615; AAF52471.1; -. PIR; A36311; A36311. HSSP; P09651; 1UP1.
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448 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CONFLICT
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Mori K., Kii S., Tsuji A., Nagahama M., Imamaki A., Hayashi K., Akamatsu T., Nagamune H., Matsuda Y.;
"A novel human PACE4 isoform, PACE4E is an active processing protease containing a hydrophobic cluster at the carboxy terminus.";
J. Biochem. 121:941-948(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=98021085; PubMed-9378725;
Tsuji A., Hine C., Tamai Y., Yonemoto K., Mori K., Yoshida S., Bando M., Saxai E., Mori K., Akamatsu T., Matsuda Y.;
"Genomic organization and alternative splicing of human PACE4 (SPC4), kexin-like processing endoprotease.";
J. Blochem. 122:438-452(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Endoprotease PACE4 is Ca2+-dependent and temperature-sensitive and can partly rescue the phenotype of a furin-deficient cell strain."; Biochem. J. 339:639-647(1999).
                                                                                                                                                                                                                 'Identification of a second human subtilisin-like protease gene in
                                                                                                                                                                                                                                                                                                                                                        Matsuda Y.; "Identification of novel cDNAs encoding human kexin-like protease,
                                                Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Identification of novel cDNAs encoding human kexin-like protease,
                                                                                                                                                                                                                                                                                                  TISSUE=Placenta;
MEDLINE=94235049; PubMed=8179631;
Tsuji A., Higashine K., Hine C., Mori K., Tamai Y., Nagamune H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isuji A., Higashine K., Hine C., Mori K., Tamai Y., Nagamune H., Matsuda Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mori K., Imamaki A., Kii S., Nagamune H., Nagahama M., Tsuji A.,
Matsuda Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORMS PACE4A-I; A-II; CS; D; E-I; E-II).
                                                                                                                                                                            Kiefer M.C., Tucker J.E., Joh R., Landsberg K.E., Saltman D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zhong M., Benjannet S., Lazure C., Munzer S., Seidah N.G.;
Functional analysis of human PACE4-A and PACE4-C isoforms:
identification of a new PACE4-CS isoform.";
FEBS Lett. 396:31-36(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Identification of a novel PACE4 isoform, PACE4E.";
Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sucic J.F., Moehring J.M., Inocencio N.M., Luchini J.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORMS PACE4E-I AND PACE4E-II).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biochem. Biophys. Res. Commun. 204:1381-1382(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                 Biochem. Biophys. Res. Commun. 200:943-950(1994).
                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORMS PACE4C AND PACE4D)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORM PACE4A-II).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALTERNATIVE SPLICING (ISOFORM PACE4CS).
                                                                                                                                                                                                                                the fes/fps region of chromosome 15.";
DNA Cell Biol. 10:757-769(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHARACTERIZATION.
MEDLINE=99233559; PubMed=10215603;
                                                                                                                                        TISSUE=Hepatoma, and Kidney;
MEDLINE=92075167; PubMed=1741956;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=95071480; PubMed=7980617;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=97335942; PubMed=9192737;
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 CONVERTASE 4) (SPC4).
                                   Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Cerebellum;
                                                                                                                                                                                                                                                                                                                                                                                              PACE4 isoforms.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PACE4 isoforms."
                                                                                        NCBI_TaxID=9606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-Placenta;
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PROCESSING
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ERRATUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matsuda
                                                                                                                                                                                               Barr
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EWBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@lsbs.ib.ch).
                ALTERNATIVE FRODUCTS: 8 ISOFORMS: PACE4A.1/PACE4 (SHOWN HERE),
PACE4A-II, PACE4B/PACE4.1, PACE4C, PACE4CS, PACE4D, PACE4E-I AND
PACE4A-II, ARE PRODUCED BY ALTERNATIVE SPLICING. ISOFORMS PACE4B,
C, CS AND D MIGHT BE ENZYMATICALLY INACTIVE.
TISSUE SPECIFICITY: EACH PACE4 ISOFORM EXHIBITS A UNIQUE
RESTRICTED DISTRIBUTION, PACE4A-I IS EXPRESSED IN HEART, BRAIN,
COMPARATIVELY HIGHER LEVELS IN THE LIVER. PACE4A-I IS AT LEAST
EXPRESSED IN PLACENTA. PACE4B WAS ONLY FOUND IN THE EMBRYONIC
KIDNEY CELL LINE FROM WHICH IT WAS ISOLATED. PACE4C AND PACE4D ARE
PLACEMENTAL PACEAE-I IS EXPRESSED IN CEREBELLUM,
PLACEMENTA. PACE4E-I IS EXPRESSED IN CEREBELLUM,
PLACEMENTA. PACE4E-I IS EXPRESSED IN CEREBELLUM,
                                                                                                                                                                                                                                                                     PROPEPTIDE CLEAVAGE AFFECTS ITS TERTIARY OR QUATERNARY STRUCTURE.
- SUBCELLULAR LOCATION: PACEAA-I AND PACEA-AII ARE SECRETED. PACEACC.
AND PACEACS ARE NOT SECRETED AND REMAIN PROBABLY IN ZYMOGEN FORM.
IN ENDOPLASMIC RETICULUM. PACEAE-I AND PACEAGE-II ARE RETAINED
INTRACELLULARLY PROBABLY THROUGH A HYDROPHOBIC CLUSTER IN THEIR C-
                                                                                                                                           AND CAPABLE OF CLEAVAGE AT THE RX(K/R)R CONSENSUS MOTIF.

1-1-CATALYTICA GATTYLTY: RELEASE OF MATURE PROTEINS FROM THEIR
PROPROTEINS BY CLEAVAGE OF ARG-AAR-YAA-ARG-1-ZAA BONDS,
WHERE XAA CAN BE ANY AMINO ACID AND YAA IS ARG OR LYS.

1-1-COFACTOR: PACEAA IS PROBABLY CALCIUM-DEPENDENT.

1-SUBUNIT: THE PACEAA I PROCUSOR PROTEIN SEEMS TO EXIST IN THE
RETICULUM ENDOPLASMIC AS BOTH A MONOMER AND A DIMER-SIZED COMPLEX
WHEREAS MATURE PACEAA-I EXISTS ONLY AS A MONOMER, SUGGESTING THAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN: THE PROPEPTIDE DOMAIN ACTS AS AN INTRAMOLECULAR CHAPERONE SSISTING THE FOLDING OF THE ZYMOGEN WITHIN THE BUDOPLASMIC RETICULUM. ISOFORM PAGE40 LACKS THE PROPEPTIDE DOMAIN. SIMILARITY: BELONGS TO PEPTIDASE FAMILY S8; ALSO KNOWN AS THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: CONTAINS 1 HOMO B/P DOMAIN.
                                                                                                                                                                                                                                                                                                                                                      TERMINUS. PACE4B MIGHT BE SECRETED.
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   MEDLINE=98408849; PubMed=9738469;
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AB001898; BAA21620.1;
AB001900; BAA21620.1;
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JOINED

BAA21622.1;

AB001914;

EMBL;

AB001909

us-09-422-838c-33.rsp

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Oliver G., Mailhos A., Wehr R., Copeland N.G., Jenkins N.A.,
                                  Development 121:4045-4055(1995).
                                                                                                                                                                                                                                                                                                                                                                                         333 AA; 35592 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                        11 AARAGGGGGGGGEGP 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                               Development.
Alternative splicing.
                                                                                                                                                                                                                                                                         SMART; SM00389; HOX; 1
                                                SEQUENCE FROM N.A.
                                                                                                                                                                PROTEINS.
                                                                                                                                                   PITUITARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 28
FXD3_CHICK
ID FXD3_CHICK
AC P79772;
                                                                                                                                                                                                                                                                                                                                                  CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
       Gruss P.;
                                                                                                                                                                                                                                                                                                                 DNA_BIND
                                                                                                                                                                                                                                                                                                                              VARSPLIC
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                      7;
                                                                                                                                                                                                                                                                                                                         Score 52.5; DB 1; Length 969; Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                      8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                  SIX3_MOUSE STANDARD; PRT; 333 AA.

062233; P70176; P70177;

01.NOV-1997 (Rel. 35, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
HOMEOBOX PROTEIN SIX3 (SINE OCULIS HOMEOBOX HOMOLOG 3).
                                                                                                                                                                                                                                                                                                                                      1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-BALB/C; TISSUE-Embryonic brain;
MEDLINE-96125147; PubMed-8575305;
                                                                                                                                                                                                                                                                                                                                                    11 AARAGGCGGGGIEGPTLR-----OWL 32
                                                                                                                                                                                                                                                                                                                                                                 24 AAGAGGAGGAGGPGFRPLAPRPWRWL 52
                                                                                                                   JOINED.
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BAA21625.1; JOINED
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Best Local Similarity 44.8%;
Matches 13; Conservative
                                                                                                                                                                         BAA21624.1;
                                                                                                                                                                                                                       BAA21624.1;
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                                                                                                                                                                                BAA21624.1
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                                                                                                                           BAA21623
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
                                                                                                                                                     AB001900;
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               AB001903;
                        AB001904;
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          AB001902;
                             AB001905
                                     AB001906
                                           AB001907
                                                         AB001914
                                                                                                                                                                         AB001903
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SIX3_MOUSE
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EMBL;
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EMBL;
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                                                                                                                                                               PSGMRSLAEPCCPTHGSAESPSTAASPTTSVSSLTERADTG
TSILSVTSSDSECDV -> ERDALPGRARLPHARLSRVTVH
GGQPDHQCVQPDGARGHRHFDPLGNLQRLGM (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: BELONGS TO THE SIX/SINE OCULIS FAMILY OF HOMEODOMAIN
"Six3, a murine homologue of the sine oculis gene, demarcates the most anterior border of the developing neural plate and is expressed during eye development.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LQHQAIGPSGMRSLAE -> SVAGTAARPPQA (IN
ISOFORM SIX3A).
MISSING (IN ISOFORM SIX3A).
G -> GG (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
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PROSITE; PS50071; HOMEOBOX_2; 1.
Developmental protein; Homeobox; DNA-binding; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 26.4%; Score 52; DB 1; Length 333; Best Local Similarity 62.5%; Pred. No. 53; Matches 10; Conservative 0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1AD7D3C4388043B9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VA -> WP (IN REF. 1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X90871; CAA62379.1; ALT_INIT.
EMBL; D83144; BAA11822.1; -.
EMBL; D83145; BAA11823.1; -.
MGD; MGI:102764; Six3.
InterPro; IPR001356; Homeobox.
Pfem; PF00046; homeobox: 1.
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0
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
FORRHEAD BOX PROTEIN D3 (HNF3/FH TRANSCRIPTION FACTOR GENESIS) (WINGED
                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                          Freyaldenhoven B.S., Freyaldenhoven M.P., Iacovoni J.S., Vogt P.K.; "Aberrant cell growth induced by avian winged helix proteins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eŭkaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Asteridae, euasterids 1; Solanales, Solanaceae, Solanum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26.4%; Score 52; DB 1; Length 394; 76.9%; Pred. No. 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00657; FORK HEAD 1; 1.
PROSITE; PS00658; FORK HEAD 2; 1.
PROSITE; PS50039; FORK HEAD 3; 1.
DNA-binding; Nuclear protein; Transcription regulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               324A4B36B9E31899 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
HOMEOBOX PROTEIN KNOTTED-1 LIKE LET12.
                                                                                                                                                                                                                                                                        Cancer Res. 57:123-129(1997).
-!- FUNCTION: PROBABLE TRANSCRIPTION FACTOR.
                                                                                                                                                                                                                                                                                                         -!- SUBCELLULAR LOCATION: NUCLEAR.
-!- SIMILARITY: CONTAINS 1 FORK-HEAD DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            426 AA
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FORK-HEAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POLY-ALA
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                                                                                                                                                                                                                         MEDLINE=97141794; PubMed=8988052;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lycopersicon esculentum (Tomato).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-CV. VFNT CHERRY;
MEDLINE-98145476; Pubmed-9484482;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001766; Fork_head.
Pfam; PF00250; Fork_head; 1.
PRINTS; PR00053; FORKHEAD.
SMART; SM00339; FH; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10; Conservative
                                                                                                 Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                 HELIX PROTEIN CWH-3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13 RAGGCCGGGGIEG 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              394 AA;
                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                              NCBI_TaxID=9031;
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                                                                                                                                                                                                             TISSUE=Embryo;
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SEQUENCE
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DOMAIN
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Matches
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                                                                                                                     Janssen B.J., Williams A., Chen J.J., Mathern J., Hake S., Sinha N., "Isolation and characterization of two knotted-like homeobox genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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NBRYOUS-SYSTEM SPECIFIC OCTAMBR-BINDING TRANSCRIPTION FACTOR N-OCT 3
(BRAIN-SPECIFIC HOMEOBOX/POU DOMAIN PROTEIN 2) (BRN-2 PROTEIN)
FOUNTRINS: N-OCT 5A; N-OCT 5B].
POUJF2 OR BRN2 OR OTF7 OR OCT7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-5580176; PubMed-7651733;
Angus J., Thomson F., Murphy K., Baker E., Sutherland G.R.,
Parsons P.G., Sturm R.A.;
"The brn-2 gene requiates the melanocytic phenotype and tumorigenic potential of human melanoma cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schreiber E., Tobler A., Malipiero U., Schaffner W., Fontana A.; Tobna cloning of human N-Oct3, a nervous-system specific POU domain transcription factor binding to the octamer DNA motif."; Nucleic Acids Res. 21:253-258(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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5B52B9E0A34A86BC CRC64;
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OC31-HUMAN STAUL...
OC31-HUMAN STAUL...
01-FEB-1991 (Rel. 17, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
...c-2001 (Rel. 40, Last annotation update)
...c-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 52; DB
Pred. No. 66;
1; Mismatches
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ELK DOMAIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00027; HOMEOBOX_1; 1. PROSITE; PS50071; HOMEOBOX_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF000142; AAC49918.1; -.
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64.78;
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Best Local Similarity 64.7
Matches 11, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8 OWLA - - ARAGGGGGGG 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     426 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                          from tomato.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-Liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
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         SO THE TENT WAS BOUNDED BY A PROPERTY AND A PROPERT
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Oncogene 11:691-700(1995).

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                                                                                                                                                                -i- SIMILARITY: STRONG TO OTHER "POU" TRANSCRIPTION FACTORS. BELONGS TO CLASS-3 POU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PSO0465; POU_2; 1.
PROSITE; PSSO071; HOMEOBOX_2; 1.
DNA-binding; Nuclear protein; Homeobox; Transcription regulation;
                                                                                                                     Treacy M.N., Simmons D.M., Ingraham H.A., Swanson L.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -> G (IN REF. 2).
2CAC852328334A66 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-OCT 3.
N-OCT 5A.
N-OCT 5B.
FOR N-OCT 5A.
FOR N-OCT 5A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POLY-GLY.
POLY-GLN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HOMEOBOX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                initiation.
                                                                                                MEDLINE-89295573; PubMed-2739723;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HOMEOBOX_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MIM, 600494;
InterPro: IPR001356; Homeobox.
InterPro: IPR000327; POU.
Pfam; PF00046; homeobox: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46921 MW;
                                                  SEQUENCE OF 280-404 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; 211933; CAA77990.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        L37868; AAB59611.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00157; pou; 1.
PRINTS; PR00028; POUDOMAIN.
ProDom; PD000583; POU; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SM00389; HOX; 1.
SMART; SM00352; POU; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Activator; Alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; S05043; S05043.
PIR; S29334; S29334.
HSSP; P14859; 1POU.
TRANSFAC; T00630; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26
443 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00027;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00035;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CELL LINEAGE.
                                                                                                                             He X., Treacy M. Rosenfeld M.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INIT_MET
INIT_MET
DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
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Gaps
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        DB 1; Length 443;
68;
                              4; Indels
          Score 52; DB
Pred. No. 68;
2; Mismatches
          26.4%;
60.0%;
Query Match
Best Local Similarity 60.v.
Best Local 9; Conservative
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26.4%; 9; Conservative · Query Match Best Local Similarity Matches ; 0 60 QWITALSHGGGGGG 74 8 QWLAARAGGGGGGG 22

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Gaps

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4; Indels

2; Mismatches

Score 52; DB 1; Length 445; Pred. No. 68;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                PROMOTERS (BY SIMILARITY).
--- SUBCELLULAR LOCATION: NUCLEAR.
--- TISSUE SPECIFICITY: EXPRESSED SPECIFICALLY IN THE NEUROECTODERMAL.
                                                         01-JUL-1993 (Rel. 26, Last sequence update)
15-JUL-1993 (Rel. 26, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
NERVOUS-SYSTEM SPECIFIC COTAMER-BINDING TRANSCRIPTION FACTOR N-OCT 3 (BRAIN-SPECIFIC HOMESDBX/POU DOMAIN PROTEIN 2) (BRN-2 PROTEIN).
                                                                                                                                                                                                                                                                                                                                            PLOG. Natl. Acad. Sci. U.S.A. 89:3280-3284(1992).
-!- FUNCTION: TRANSCRIPTION FACTOR THAT BINDS PREFERENTIALLY TO THE RECOGNITION SEQUENCE WHICH CONSISTS OF TWO DISTINCT HALF-SITES, ('GCAT') AND ('TAAT'), SEPRATED BY A NONCONSERVED SPACER REGION OF 0, 2, OR 3 NUCLEOTIDES. POSITIYELY REGULATES THE GENES UNDER THE CONTROL OF CORTICOTROPIN-RELEASING HORMONE (CRH) AND CRH II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: STRONG TO OTHER "POU" TRANSCRIPTION FACTORS. BELONGS TO CLASS-3 POU.
                                                                                                                                                                                                                                                                                               Hara Y., Rovescalli C., Kim Y., Nirenberg M.; Structure and evolution of four POU domain genes expressed in mouse
                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mommalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA-binding; Nuclear protein; Homeobox; Transcription regulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     47149 MW; 1A47F10950EECE8A CRC64;
                               445 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POLY-GLN.
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                                                                                                                                                                                                                                                                               MEDLINE=92228768; PubMed=1565620;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS50027; HOMEOBOX_1; 1. PROSITE; PS50071; HOMEOBOX_2; 1.
                                                                                                                                                 POUGE2 OR OTF7 OR BRN2 OR BRN-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; S31224; S31224.
HSSP; P14859; 1P00.
MGD: MGI:101895; P00312.
InterPro; IPR001356; Homeobox.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00046; homeobox; 1.
Pfam; PF00157; pou; 1.
PRINTS; PR00028; POUDOMAIN.
ProDom; PD000583; POU; 1.
SMART; SM0389; HOX; 1.
SMART; SM00352; POU; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M88300; AAA39961.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PS00035; POU_1; 1.
PS00465; POU_2; 1.
                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90
149
338
                                                                                                                                                                 Mus musculus (Mouse).
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125
268
356
445 AA;
                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CELL LINEAGE.
                                                                                                                                                                                                                                                                    TISSUE=Brain;
                                 OC3N_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Activator.
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DNA_BIND
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE;
                                                                                                                                                                                                                                                                                                                                       brain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
RESULT 31
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                                                                                                                                                                                                                                                                                                                                            MEDLINE-91184140; Pubmed=2009862;
Mohun T.J., Chambers A.E., Towers N., Taylor M.V.;
Mohun T.J., Chambers A.E., Towers N., Taylor M.V.;
Expression of genes encoding the transcription factor SRF during early development of Xenopus laevis: identification of a Carg EMBO J. 10:933-940(1991).

-!- ENBO J. 10:933-940(1991).

-!- FUNCTION: SRF IS A TRANSCRIPTION FACTOR THAT BINDS TO THE SERUM RESPONSE ELEMENT (SRE). A SHORT SEQUENCE OF DYAD SYMMETRY LOCATED 300 BP TO THE 5' OF THE SITE OF TRANSCRIPTION INITIATION OF SOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SUBUNIT: BINDS DNA AS A MULTIMER, PROBABLY A DIMER.
-!- SUBCELLULAR LOCATION: NUCLEAR.
-!- PTW: PHOSPHORYLATED (PROBABLE).
-!- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ranscription regulation; DNA-binding; Activator; Nuclear protein;
                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
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68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B3CDCA7E0D97C23B CRC64;
                                                                                                                                                                    01-NOV-1991 (Rel. 20, Last sequence update)
01-OCT-1994 (Rel. 30, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             462 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26.4%; Score 52;
64.7%; Pred. No.
                                                                                                                                                                                                                            Kenopus laevis (African clawed frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MADS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00350; MADS_BOX_1; 1.
PROSITE; PS50066; MADS_BOX_2; 1.
                                                                                                                                                      01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sego
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP; P11831; 1SRS.
TRANSFAC; T00763; -
InterPro; IPR002100; MADS-box.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46115 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X56451; CAA39832.1; -. PIR; S15018; S15018.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRO0404; MADSDOMAIN.
                                                                                                                                                                                                          SERUM RESPONSE FACTOR (SRF)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10 LAARAGGGGGGGGIEGP 26
                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18 LARRAGNGAGCPGIRGP 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
8 QWLAARAGGGGGGG 22
                                60 QWITALSHGGGGGG 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00319; SRF-TF;
                                                                                                                                                                                                                                                                             Kenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE 448 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Phosphorylation.
                                                                                                                                                                                                                                                                                               NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SM00432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FACTORS.
                                                                                                                   SRF_XENLA
P23790;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ERR1_MOUSE
008580;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS;
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                                                                                                     SRF_XENLA
                                                                                                                                    qq
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                                                                                                                                                                                                                                                                                                                                                                                                                                            AMEDIUM-CHAIN AST AN IMPORTANT REGILATOR (MAD) THE MOUSE ELEMENT (ERRE) CONTAINING A SINGLE CONSENSUS HALF-STIE, S'TNAAGGTCA-3', CAN BIND TO THE MEDIUM-CHAIN ACTL COGNENSUR A BETTOROGENESE (MCAD) RESPONSE ELEMENT (ERRE) CONTAINING A SINGLE CONSENSUS HALF-STIE, S'TNAAGGTCA-3', CAN BIND TO THE MEDIUM-CHAIN ACYL COGNEYME A DEHYDROGENASE (MCAD) RESPONSE ELEMENT REGILATOR OF MCAD PROMOTER. WRRE-1 AND MAY ACT AS AN IMPORTANT REGILATOR OF MCAD PROMOTER. MAY FUNCTION AS A MODULATOR OF THE ESTROGEN SIGNALING PATHWAY IN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBULIT: BINDS DNA AS A MONOMER (PROBABLE).
SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
IISSUE SPECIFICITY: MOST HIGHLE EXPRESSED IN KIDNEY, HEART, AND
BROWN ADIPOCYTES. ALSO FOUND IN UTERUS, CERVIX AND VAGINA.
DEVELOPMENTAL STAGE: EXPRESSED IN AN ORGAN SPECIFIC MANNER THROUGH
MID-TO LARTE EMBRYONIC DEVELOPMENT WITH PRESISTERT HIGH-LEVEL
EXPRESSION IN BROWN ADIPOSE TISSUE AND INTESTINAL MUCOSA.
INDUCTION: ACTIVATED BY DIETHYLSTILBESTROL (DES) AND ESTRADIOL IN
                                                                                                                                                                                                                                                                         Sladek R., Bader J. A., Giguere V., The orphan nuclear receptor estrogen-related receptor alpha is a transcriptional regulator of the human medium-chain acyl coenzyme
                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00430; HOLI; 1.
SMART; SM00390; ZnF_C4; 1.
PROSTIE; PS00031; NUCLEAR_RECEPTOR; 1.
Receptor; Transcription regulation; DNA-binding; Nuclear protein; Zinc-finger; Phosphorylation.
15-JUL-1999 (Rel. 38, Created)
20-AGG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
STEROID HORMONE RECEPTOR ERRI (ESTROGEN-RELATED RECEPTOR, ALPHA)
(ERR-ALPHA) (ESTROGEN RECEPTOR-LIKE 1) (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIM: PHOSPHORYLATED (PROBABLE).
SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
NR3 SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEAR RECEPTOR-TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MGD; MGI:1346831; ESTTA.
In:erPro; IPR000336; Hormone_rec_lig.
Interpro; IPR001723; Strdhormone_roptor.
Interpro; IPR001723; Strdhormone_roptor.
Pfam; PF00104; hormone_rec; 1.
Pfam; PF00105; Ef-C4; I.
PRINTS; PR00047; STROIDFINGER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C4-TYPE.
C4-TYPE.
                                                                                                                                                                                                                                                                                                                                                     Mol. Cell. Biol. 17:5400-5409(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U85259; AAB51250.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
TISSUE-Brain, and Kidney;
MEDLINE-98121983; PubMed-9460651;
                                                                                                                                                                                                                                                          MEDLINE=97415618; PubMed=9271417;
                                                                                                     ESPRA OR NR3B1 OR ERR1 OR ESTRRA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR00398; STRDHORMONER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         184
139
179
                                                                                                                         Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                       dehydrogenase gene.
                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                  NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    THE UTERUS.
                                                                                                                                                                                                                                        STRAIN-BALB/C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                UTERUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA_BIND
ZN_FING
ZN_FING
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Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cole S.T., Brosch K., Parklill J., Garnier T., Churcher C., Harris D., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quali M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Shelton S., Squares S., Squares R., Deciphering the biology of Mycobacterium tuberculosis from the Complete genome sequence.";

Nature 393:537-544(1998).
                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-MAY-2000 (Rel. 39, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
GLUTAMYL-TRNA(GLN) AMIDOTRANSFERASE SUBUNIT A (EC 6.3.5.-) (GLU-ADI
                                                                                                                                                     .;
0
                                                                                     26.4%; Score 52; DB 1; Length 462; 62.5%; Pred. No. 70; cive 0; Mismatches 6; Indels
462 AA; 49280 MW; EE70CB37F435BE00 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RV3011C OR MT3091 OR MTV012.25C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=98295987; PubMed=9634230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AL021287; CAA16096.1; -. EMBL; AE007128; AAK47420.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-MAY-2000 (Rel. 39, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mycobacterium tuberculosis.
                                                                                                                        Best Local Similarity 62.5
Matches 10; Conservative
                                                                                                                                                                                                                     11 AARAGGGCGGGGIEGP 26
                                                                                                                                                                                                                                                                           2 AARRGGAAGGGGPRSP 17
                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                             GATA_MYCTU
O53258;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBUNIT A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bishai W.;
         SEQUENCE
                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GATA OR
                                                                                                                                                                                                                                                                                                                                                                       RESULT 34
                                                                                                                                                                                                                                                                                                                                                                                                       GATA_MYCTU
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TIGR; MT3091;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -1: DEVELOPMENTAL STAGE: CLN1 AND CLN2 MRNAS FLUCTUATE PERIODICALLY IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Messenguy F., Dubois E., Vierendeels F., Scherens B.;
Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE G1/S
(START) TRANSITION. INTERACTS WITH THE CDC28 PROTEIN KINASE TO
                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleotide sequence of the Saccharomyces cerevisiae CLN1 and CLN2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE-89345642; PubMed=2569741;
Hadwiger J.A., Wittenberg C., Richardson H.E., de Barros Lopes M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Reed S.I.;
As family of cyclin homologs that control the G1 phase in yeast.";
Proc. Natl. Acad. Sci. U.S.A. 86:6255-6259(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: BELONGS TO THE CYCLIN FAMILY. STRONGEST TO OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Saccharomyces cerevisiae (Baker's yeast).
Eukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes;
Saccharomycetales, Saccharomycetaceae, Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                     ;;
0
                                                                                                                                                                                                                                                                                       Query Match 26.4%; Score 52; DB 1; Length 494; Best Local Similarity 52.6%; Pred. No. 74; Matches 10; Conservative 0; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wittenberg C., Chapman-Shimshoni D.;
Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                  M -> L (IN REF, 2),
; 99A8824ABC436CA6 CRC64;
                                                                                                                                      Protein biosynthesis; Ligase; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-FEB-1991 (Rel. 17, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-CCT-1996 (Rel. 34, Last annotation update)
01/S-SPECIFIC CYCLIN CLN2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              545 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic Acids Res. 18:4025-4025(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=90326560; PubMed=2197605;
                            InterPro; IPR000120; Amidase, pfam; PF01425; Amidase; 1 PROSITE; PS00571; AMIDASES; 1.
                                                                                                                                                                  420 420 M
494 AA; 51438 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           141 GPTRNPWNLDRVPGGSGGG 159
                                                                                                                                                                                                                                                                                                                                                                                                                                        .3 GPTLRQWLAARAGGGCGG 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
Tuberculist; Rv3011c; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hadwiger J.A., Reed S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLN2 OR YPL256C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FORM MPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIGNALS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CG12_YEAST
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                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                         CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  genes.
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CGG13_YEAST

CGG13
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4D7189B83D7A2B34 CRC64;

Cyclin; Cell cycle; Cell division. SEQUENCE 546 AA; 62049 MW; 4D7

Pfam; PF00134; cyclin; 1. SMART; SM00385; CYCLIN; 1. PROSITE; PS00292; CYCLINS; 1.

SGD; S0004812; CLN1. InterPro; IPR000553; Cyclin.

M33264; AAA65724.1; -. Z47815; CAA87822.1; -.

EMBL; EMBL;

COBYCI

PIR; A33289;

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Gaps
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Submitted (JAN-1985) to the ENRL/Genenk/DDBD databases.
-!- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE G1/S
(START)_TRANSITION: INTERACTS WITH THE CDC28 PROFEIN KINASE TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- DEVELOPMENTAL STAGE: CLN1 AND CLN2 MRNAS FLUCTUATE PERIODICALLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hadwiger J.A., Reed S.I.; "Nucleotide sequence of the Saccharomyces cerevisiae CLN1 and CLN2 ^{\circ}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "A family of cyclin homologs that control the G1 phase in yeast."; Proc. Natl. Acad. Sci. U.S.A. 86:6255-6259(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hadwiger J.A., Wittenberg C., Richardson H.E., de Barros Lopes M., Reed S.I.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              THE CELL CYCLE, PERKING IN G1 PHASE.

-!- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. STRONGEST TO OTHER G1/S CYCLINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                  10;
                                                                                                                                                                                 26.4%; Score 52; DB 1; Length 545; 38.7%; Pred. No. 81;
                                                                                                                                                                                                                8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wittenberg C., Chapman-Shimshoni D.;
Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                    D6426B94E040E960 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                             (Rel. 33, Last sequence update)
(Rel. 34, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                     546 AA
                                                                                                                                                                                                               1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                      125 WLAAKTWGGCNHIINNVVIPTGGRFYGPNPR 155
                                                                                                                                                                                                                                           9 WLAARAGGCCG-----GGGIEGPTLR 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic Acids Res. 18:4025-4025(1990)
                                                                     Pfam; PF00134; cyclin; 1.
SMART; SM00385; CYCLIN; 1.
SMOSITE; PS00292; CYCLINS; 1.
CYCLIN; Cell Gycle; Cell division.
SEQUENCE 545 AA; 61696 MW; D64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE-90326560; PubMed=2197605;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-89345642; PubMed-2569741;
                                                                                                                                                                                                                                                                                                                                                                             01-FEB-1991 (Rel. 17, Created)
EMBL; M33265; AAA65725.1; -. EMBL; Z73612; CAA97982.1; -.
                          PIR; B33289; COBYC2.
SGD; S0006177; CLN2.
InterPro; IPR000553; Cyclin.
                                                                                                                                                                                                                                                                                                                                                                                                                                        CLN1 OR YMR199W OR YM9646.13.
                                                                                                                                                                                             Local Similarity 38.7 es 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-1996 (Rel. 34, Las
G1/S-SPECIFIC CYCLIN CLN1
                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=S288C / AB972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID-4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FORM MPF
                                                                                                                                                                                                                                                                                                                                                 CG11_YEAST
P20437;
                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-1996
                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REVISIONS
                                                                                                                                                                                               Best Loca
Matches
                                                                                                                                                                                                                                                                                                                    RESULT 36
CG11_YEAST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-1996 (Rel. 34, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
CAMP-DEPENDENT 3',5'-CYCLIC PHOSPHODIESTERASE (EC 3.1.4.17) (LEARNING/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- ALTERNATIVE PRODUCTS: DIFFERENT FORMS ARE GENERATED BY THE USE OF DIFFERENT TRANSCRIPTION START SITES AND SPLICE PATTERNS.
-!- DISEASE: MUTATION OF DUNCE PRODUCES FEBALE FLIES THAT ARE STERILE.
-!- SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera: Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                coding sequences of the Drosophila dunce+ gene, the structural gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      for cAMP phosphodiesterase.";
Proc. Natl. Acad. Sci. U.S.A. 83:9313-9317(1986).
-1- CATALYTIC ACTIVITY: ADENOSINE 3',5'-CYCLIC PHOSPHATE + H(2)0 =
ADENOSINE 5'-PHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chen C.-N., Denome S., Davis R.L.; "Molecular analysis of cDNA clones and the corresponding genomic
                                                                                    10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oiu Y.H., Chen C.-N., Malone T., Richter L., Beckendorf S.K., Davis R.L.;
       Score 52; DB 1; Length 546;
Pred. No. 81;
1; Mismatches 8; Indels
                                                                                8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Characterization of the memory gene dunce of Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                584 AA
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                                                                                                                                                                                                                   123 WLAAKTWGGCNHIINNVSIPTGGREYGPNPR 153
                                                                                                                                                  9 WLAARAGGGCG------GGGIEGPTLR 29
                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., AND REVISIONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 223-584 FROM N.A. MEDLINE=87092243; PubMed=3025834;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=92085274; PubMed=1660926;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mol. Biol. 222:553-565(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-1989 (Rel. 12, Created)
       26.48;
38.78;
Query:Match 26.4
Best Local Similarity 38.7
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEMORY PROCESS PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBUNIT: MONOMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=CANTON-S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             melanogaster."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DUNCE OR DNC
                                                                                                                                                                                                                                                                                                                                                                                                         CNA1_DROME
P12252;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FAMILY
                                                                                                                                                                                                                                                                                                                                                                          CNA1_DROME
                                                                                                                                                                                                                                                                                                                                       RESULT
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EMBL; X55167; CAA38960.1; -. EMBL; X55168; CAA38960.1; JOINED.

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us-09-422-838c-33.rsp

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DOMAIN 305 310 PART OF CAMP BINDING SITE (BY SIMILARITY
TO MAMALLAN REGULATORY SUBUNIT OF TYPE 2
CAMP DEPENDENT PROTEIN KINASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Darmon M.Y., Semat A., Darmon M.C., Vasseur M.; "Sequence of a cDNA encoding human keratin No 10 selected according to structural homologies of keratins and their tissue-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDILINE-89125611; Pubmed-2464696;
Rieger M., Franke W.W.; Propertion of an orthologous mammalian cytokeratin gene. High degree of intron sequence conservation during evolution of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata; Craniata; Vertebrata, Euteleostomi,
Mammalia; Eutheria; Primates; Catarrhini, Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 197-593 FROM N.A. MEDLINE-92339897; PubMed-1378806; Trachenko A.V., Buchman V.L., Bliskovsky V.V., Shvets Y.P., "Kisselev L.L.; "Kisselev L.L.; "Exons I and VII of the gene (Kerl0) encoding human keratin 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JAN-1990 (Rel. 13, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
KERATIN, TYPE I CYTOSKELETAL 10 (CYTOKERATIN 10) (K10) (CK 10).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99239BE33C620501 CRC64;
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                                                                                                                    JOINED.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00126; PDEASE_I; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64875 MW;
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                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR003607; HDc.
InterPro; IPR002073; PDEase.
                                                                                                                                                                                                                                                                                                                         FlyBase; FBgn0000479; dnc.
CAA38960.1;
CAA38960.1;
                                              CAA38960.1;
                                                                                                                                                                                                                                              AAC34201.1;
AAC34201.1;
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AAC34201.1;
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Matches 11; Conservative
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559
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M14981;
                                                 x55171;
                                                                        x55172;
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MEDLINE-95059228; PubMed-7526210;
Paller A.S., Syder A.J., Chan Y.-M., Yu Q.-C., Hutton M.E., Tadini G.,
                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=92141228; PubMed=1371013; Korge B.P., Steinert P.M.; Korge B.P., Gan S.-Q., McBridge O.W., Mischke D., Steinert P.M.; "Extensive size polymorphism of the human keratin 10 chain resides in the C-terminal V2 subdomain due to variable numbers and sizes of glycine loops.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=94216497; PubMed=7512983; Syder A.J., Yu Q.-C., Paller A.S., Giudice G., Pearson R., Fuchs E.; "Genetic mutations in the K1 and K10 genes of patients with epidermolytic hyperkeratosis. Correlation between location and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               McLean W.H.I., Eady R.A.J., Dopping-Hepenstal P.J.C., McMillan J.R.,
Leigh I.M., Navsaria H.A., Higgins C., Harper J.I., Paige D.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rothnagel J.A., Dominey A.M., Dempsey L.D., Longley M.A., Greenhalgh D.A., Gagne T.A., Huber M., Frenk E., Hohl D., Roop D.R.; "Mutations in the rod domains of keratins 1 and 10 in epidermolytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VARTANTS EHK HIS-154; CYS-156; HIS-156; ASP-160 AND GLN-442.
MEDLINE-94136477; PubMed-7508181;
Chipev C.C., Yang J.-M., Digiovanna J.J., Steinert P.M., Marekov L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Compton J.G., Bale S.J.; "Preferential sites in keratin 10 that are mutated in epidermolytic
                                                                                                                                                   "Microsequences of 145 proteins recorded in the two-dimensional gel
protein database of normal human epidermal keratinocytes.";
Electrophoresis 13:960-969(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rothmagel J.A., Longley M.A., Holder R.A., Kuster W., Roop D.R.; "Prenatal diagnosis of epidermolytic hyperkeratosis by direct gene
                                                                                                                                                                                                                                                                          Cheng J., Syder A.J., Yu Q.-C., Letal A., Paller A.S., Fuchs E., "The genetic basis of epidermolytic hyperkeratosis: a disorder of differentiation-specific epidermal keratin genes."; Cell 70:811-819(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fuchs E.; "Genetic and clinical mosaicism in a type of epidermal nevus."; New Engl. J. Med. 331:1408-1415(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Morley S.M.; "Mutations in the rod 1A domain of keratins 1 and 10 in bullous congenital ichthyosiform erythroderma (BCIE)."; J. Invest. Dermatol. 102:24-30(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VARIANTS EHK ARG-150; CYS-156 AND GLU-439, AND VARIANT SER-126
                                                                                                                  Rasmussen H.H., van Damme J., Puype M., Gesser B., Celis J.E.,
undergo structural rearrangements within repeats.";
Gene 116:245-251(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 89:910-914(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequencing.";
J. Invest. Dermatol. 102:13-16(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        disease severity.";
J. Clin. Invest. 93:1533-1542(1994).
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MEDLINE=94117870; PubMed=7507152;
                                                                                                                                                                                                                                          VARIANT EHK HIS-156.
MEDLINE=92386600; PubMed=1381287;
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                                                                                                 MEDLINE-93162043; PubMed=1286667;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VARIANTS EHK HIS-156 AND SER-161.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VARIANT EHK ASN-160.
MEDLINE-94117868; PubMed=7507150;
                                                            SEQUENCE OF 180-184 AND 577-589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hyperkeratosis.";
Science 257:1128-1130(1992).
                                                                              TISSUE=Keratinocytes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VARIANT EHK THR-150.
                                                                                                                                         Vandekerckhove J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hyperkeratosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- POLYMORPHISM: A NUMBER OF ALLELES ARE KNOWN THAT MAINLY DIFFER IN THE GLY-RICH REGION (POSITIONS 490-560).
-!- DISEASE: DEPERCYS IN KRY10 ARE THE CAUSE OF EPIDERWOLYTIC HYPERKERATOSIS (EHK) (ALSO KNOWN AS BULLOUS CONGENITAL ICHTHYOSIFORM ERYTHRODERMA (BCIE)); A HEREDITARY SKIN DISORDER CHARACTERIZED BY BLISTERING AND A MARKED THICKENING OF THE STRATUM CORNEUM. AT BIRTH, AFFECTED INDIVIDUALS USUBLIX PRESENT WITH REDNESS, BLISTERS AND SUPERFICIAL EROSIONS DUE TO CYTOLYSIS. WITHIN A FEW WEEKS, THE ERYTHRODERMA AND BLISTER FORMATION DIMINISH AND HYPERREATOSES DEVELOP. TRANSMISSION IS AUTOSOMAL
                                                                                                                                                                                                                                                                                                                                                                                  Arin M.J., Longley M.A., Anton-Lamprecht I., Kurze G., Huber M., Hohl D., Rothnagel J.A., Roop D.R.;
"A novel substitution in keratin 10 in epidermolytic hyperkeratosis.";
J. Invest. Dermatol. 112:506-508(1999)
-!- SUBUNI: HETEROTETRAME NO TWO TYPE I AND TWO TYPE II KERATINS.
KERATIN 10 IS GENERALLY ASSOCIATED WITH KERATIN 1.
-!- TISSUE SPECIFICITY: SEEN IN ALL SUPRABASAL CELL LAYERS INCLUDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMINANT, BUT MOST CASES ARE SPORADIC.
DISRASE: DEFECTS IN KRT10 ARE THE CAUSE OF ANNULAR EDIDERMOLYTIC
ICHTHYOSIS (AEI), A DISTINCT PHENOTYPIC VARIANT OF EDIDERMOLYTIC
HYPERKERAPOSIS. IT RESEMBLES CLINICAL AND HISTOLOGIC FEATURES OF
BOTH EPIDBERMOLYTIC HYPERKERATOSIS AND ICHTHYOSIS BULLOSA OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MISCELLANBOUS: THERE ARE TWO TYPES OF CYTOSKELETAL AND MICROFIBRILLAR KERATIN: I (ACIDIC; 40-55 KDA) [K9 TO K20] AND II (NEUTRAL TO BASIC; 56-70 KDA) [K1 TO K8].

SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT FAMILY.
CAUTION: REF. 2 SEQUENCE DIFFERS FROM THAT SHOWN EXTENSIVELY IN POSITIONS 513 TO 555.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00226; IF; 1.
Intermediate filament; Coiled coil; Keratin; Disease mutation;
                                                              MEDLINE=99072665; PubMed=9856845; Suga Y., Duncan K.O., Heald P.W., Roop D.R.; A novel helix termination mutation in keratin 10 in annular epidermolytic ichthyosis, a variant of bullous congenital ichthyosiform erythroderma.";
                                                                                                                                                                                                                                                  J. Invest. Dermatol. 111:1220-1223(1998)
                                                                                                                                                                                                                                                                                                                    VARIANT EHK SER-160.
MEDLINE-99215719; PubMed-10201536;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001664; IF.
InterPro; IPR002957; Keratin_I.
Pfam; PF00038; filament; 1.
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Aarhus/Ghent-2DPAGE; 7405; IEF
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PRINTS; PR01248; TYPE1KERATIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M19156; AAAS9468.1; --
EMBL; M77663; AAAS9199.1; --
EMBL; L20218; AABS9438.1; --
EMBL; L20219; AABS9439.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X14487; CAA32649.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRATUM CORNEUM.
[13]
VARIANT AEI THR-446.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MIM; 148080; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIEMENS
                                                                                                                                                                                                                                                                           14]
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   RANGE STATE STATE
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TAIL.
COIL 1A.
LINKER 1.
COIL 1B.
LINKER 12.

145 456 593 181 202 294

Polymorphism.

DOMAIN DOMAIN DOMAIN DOMAIN DOMAIN

COIL 2. GLY/PHE/SER-RICH. GLY/SER-RICH. G -> S. /FTIG-VAR_010505. M -> R (IN EHK). /FTIG=VAR_010506. M -> T (IN EHK). /FTIG=VAR_010507. N -> H (IN EHK). /FTIG=VAR_010507. N -> H (IN EHK). /FTIG=VAR_0103826. R -> H (IN EHK). /FTIG=VAR_013827. R -> C (IN EHK). /FTIG=VAR_013828. R -> P (IN EHK). /FTIG=VAR_013828. R -> P (IN EHK). /FTIG=VAR_013828. R -> C (IN EHK). /FTIG=VAR_013829. R -> D (IN EHK). /FTIG=VAR_013829. R -> D (IN EHK). /FTIG=VAR_01383. Y -> D (IN EHK).	; Score 52; DB 1; Length 593; ; Pred. No. 87; 5; Mismatches 5; Indels 0; Gaps (	Araca Standard, Prt; 1168 AA.  PHOSES, ACCA STANDARD; PRT; 1168 AA.  PHOSES, ACCA STANDARD; PRT; 1168 AA.  PHOSES, ACCACA STANDARD; PRT; 1168 AA.  PHOSES, ACCACACACACACACACACACACACACACACACACACA
456 1446 590 126 150 150 156 156 156	tch 26.4%; al Similarity 47.4%; 9; Conservative ROWLAARAGGGGGGGGG 25::::::	ACACA MYSC_ACACA ACACA ACACA ACACA BIOL-1989 (Rel. 11, Last sequence 10-JUL-1989 (Rel. 11, Last sequence 20-AUG-2001 (Rel. 40, Last annotatio MYCOSIN IC HEAVY CHAIN. MYCOSIN IC HEAVY CHAIN. ACANTHAMOEDA CASTEllanii (Amoeba). BUKHI_TAXID=5755. BEQUENCE FROM N.A. MEDLINE-88016163; PubMed=3477803; JUNG G., Korn E.D., Hammer J.A. III; "The heavy captain of Acanthamoeba myo and non-myosin-like sequences." Proc. Natl. Acad. Sci. U.S.A. 84:672 [2] PARTIAL SEQUENCE FROM N.A. MEDLINE-86259656; PubMed=3014500; Hammer J.A. III, Jung G., Korn E.D.; Hammer J.A. III, Jung G
318 451 126 150 150 154 156 156 156	Similarity 9; Conser NLAARAGGGGG :: :	2A ST. 989 (Rel. 989 (Rel. 001 (Rel. 001 (Rel. 101 (Rel. 102 (Rel. 103 (Rel.
DOMAIN DOMAIN DOMAIN VARIANT VARIANT VARIANT VARIANT VARIANT	Query Match Best Local Si Matches 7 RQWLA 7 RCWLA 9 HYSS	AACAGA MASS MASS MASS MASS MASS MASS MASS M
	. Qu Be Ma Ma Db	MYSCLAS CO D D D D D D D D D D D D D D D D D D

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                           MISCELLANEOUS: THIS ORGANISM EXPRESSES AT LEAST THREE ISOFORMS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J. Bacteriol. 175:2379-2392(1993). -1- CATALYTIC ACTIVITY: 3 NAD(P)H + NITRITE = 3 NAD(P)(+) + NH(4)OH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Frozon; PD000355; M.Z.
SMART; SM00242; MYSC; 1.
SMART; SM00242; MYSC; 1.
SMART; SM00242; SH3; 1.
SMOSITE; PS50002; SH3; 1.
MYOSIN; ATP-binding; Phosphorylation; Multigene family; SH3 domain.
DOMAIN; 1 670
TAIL HOMOLOGY REGION 1 (TH.1).
GTS GTY/PRO/ALA-RICH (TH.2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- COFACTOR: THIS ENZYME IS A FAD FLAVOPROTEIN THAT ALSO CONTAINS A SIROHEME AND ONE 2FE-2S IRON-SULFUR CENTER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Molecular cloning, characterization, and nucleotide sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nit-6, the structural gene for nitrite reductase in Neurospora crassa.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
                         MYOSIN I HEAVY-CHAIN, ENCODED BY GENES MIA, MIB, AND MIC.
--- SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
---- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
---- CAUTION: WAS ORIGINALLY THOUGHT TO BE MYOSIN IB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26.4%; Score 52; DB 1; Length 1168; 55.0%; Pred. No. 1.5e+02; ive 2; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      D07084B373A37A32 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GLY/PRO/ALA-RICH (TH.2).
ATP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
12-UL-1999 (Rel. 38, Last annotation update)
NITRITE REDUCTASE [NAD(P)H] (EC 1.6.6.4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PHOSPHORYLATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sordariales; Sordariaceae; Neurospora
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP; PO8799; IMND.
InterPro; IPR001452; SH3.
InterPro; IPR001609; myosin_head.
Pfam; PF00063; myosin_head; 1.
Pfam; PF00018; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS: PR00193; MYOSINHEAVY.
PRINTS: PR00452; SH3DOMAIN.
ProDom; PD000355; myosin_head; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=74-OR23-1A;
MEDLINE=93224461; PubMed=8096840;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   920 QILGAKGGGGGGGRGRGGPS 939
                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; J02974; AAA27707.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 OWLAARAGGGCGGGGIEGPT 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         127309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 55.0'
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1168
108
311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; A33891; MWAXIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1168 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Neurospora crassa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=5141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NIR_NEUCR
P38681;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      H(2)0
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NIR_NEUCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a
SOUTH THE TENT TO 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
Panicoideae; Andropogoneae; Sorghum.
                                                                                                                                                                                                                                                                          InterPro; IPR001327; FAD_pyr_redox.
InterPro; IPR000650; Nir_Sir.
Pfam; PF01077; NIR_SIR; 1.
Pfam; PF00070; pyr_redox; 1.
PR01175; PR00397; SIRCHARM.
PROSTIE; PS00365; NIR_SIR; 1.
Oxidoreductase; FAD; Flavoprotein; Iron-sulfur; Nitrate assimilation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
-!- PATHWAY: SECOND STEP IN NITRATE ASSIMILATION (DENITRIFICATION).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-CV. 58M;
MEDLINE-20188796; PubMed=10723737;
Alba R., Kelmenson P.M., Cordonnier-Pratt M.-M., Pratt L.H.;
"The phytochrome gene family in tonname";
             -i- SUBUNIT: HOMODIMER (BY SIMILARITY).
-i- INDUCTION: BY NITRATE.
-i- SIMILARITY: THE C-TERMINAL DOMAIN IS A 4FE-4S/SIROHEME DOMAIN
FOUND IN MITRITE REDUCTASES (EC 1.6.6.4 AND EC 1.7.7.1) AND
SULFITE REDUCTASES (EC 1.8.1.2 AND EC 1.8.7.1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                          (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AND SIROHEME
                                                                                                                                                                                                                                                                                                                                                                                                                                           (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=CV. 58M;
MEDLINE=97198556; PubMed=9046599;
Chlids K.L., Miller F.R., Cordonnier-Pratt M.-M., Pratt L.H.,
Morgan P.W., Mullet J.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 52; DB 1; Length 1176; Pred. No. 1.6e+02; 1ndels 4; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FFC7DCE66F80C710 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                         FAD (POTENTIAL).
NAD(P)H (POTENTIAL).
IRON-SULFUR (2FE-2S) (IRON-SULFUR (2FE-2S) (IRON-S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sorghum bicolor (Sorghum) (Sorghum vulgare).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT; 1178 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 evolution of this family in angiosperms."; Mol. Biol. Evol. 17:362-373(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRO/SER-RICH
                                                                                                                                                                                                                                             EMBL; L07391; -; NOT_ANNOTATED_CDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        998 1054 PRO
1176 AA; 127367 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 208-1178 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26.4%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ::: | |||||| |:|
115@ KKLVEAVGGGCGGGGLE 1175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 ROWLAARAGGGGGGGIE 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 50, vv
Best Local 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                          60
215
717
723
757
761
                                                                                                                                                                                                                                                             PIR; A49848; A49848.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                            26
183
717
723
757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=4558;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PHYTOCHROME B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PHYB OR MA3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PHYB_SORBI
                                                                                                                                                                                                                                                                                                                                                                                             Heme; NADP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                          NP_BIND
NP_BIND
METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                              METAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                               FUNCTION: REGULATORY PHOTORECEPTOR WHICH EXISTS IN TWO FORMS THAT ARE REVERSIBLY INTERCONVERTIBLE BY LIGHT: THE PR FORM THAT ABSORBS MAXIMALLY IN THE RED REGION OF THE SPECTRUM AND THE PER FORM THAT ABSORBS MAXIMALLY IN THE FAR-RED REGION. PHOTOCONVERSION OF PR IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
UI SMALL NUCLEAR RIBONUCLEOPROTEIN 70 KDA (UI SNRNP 70 KDA) (SNRNP70)
                                                                                                                                                                                       BISHOSPHATE CARBOXXIASE, CHLCROPHYLL A/B BINDING PROTEIN, PROTOCHLOROPHYLLIDE REDUCTASE, RRNA, ETC. IT ALSO CONTROLS THE EXPRESSION OF ITS OWN GENE(S) IN A NEGATIVE FEEDBACK FASHION (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transcription regulation; Photoreceptor; Phytochrome; Chromophore; Multigene family.
The sorghum bicolor photoperiod sensitivity gene, Ma3, encodes a
                                                                                                                     PER INDUCES AN ARRAY OF MORPHOGENIC RESPONSES, WHEREAS RECOVERSION OF PER TO PR CANCELS THE INDUCTION OF THOSE MESPONSES. PER COUTREOLS THE EXPRESSION OF A NUMBER OF NUCLEAR GENES INCLUDING THOSE ENCODING THE SMALL SUBUNIT OF RIBULOSE.
                                                                                                                                                                                                                                                            SUBUNIT: HÓMODIMER (BY SIMILARITY).
PTM: CONTAINS ONE COVALENTLY LINKED TETRAPYRROLE CHROMOPHORE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26.4%; Score 52; DB 1; Length 1178; 68.8%; Pred. No. 1.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POLY-GLY.
CHROMOPHORE (BY SIMILARITY).
W: C406DF221197B93F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Indels
                                                                                                                                                                                                                                                                                                SIMILARITY: BELONGS TO THE PHYTOCHROME FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POLY-HIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00245; PHYTOCHROME_1; 1.
PROSITE; PS50046; PHYTOCHROME_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF182394; AAB41398.2; -.
InterPro; IPR000410; Bctrl_sensor.
InterPro; IPR003018; GAF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR003594; HATPase_c.
InterPro; IPR003661; His_kinA.
InterPro; IPR000014; PAS.
InterPro; IPR001294; Phytochrome.
Pfam; PF01590; GAF; 2.
Pfam; PF02518; HATPase_c; 1.
                phytochrome B.";
Plant Physiol. 113:611-619(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                129136 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PF00360; phytochrome; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00065; GAF; 1.
SMART; SM00387; HATPASe_C; 1.
SMART; SM00388; Hiska; 1.
SMART; SM00091; PAS; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR01033; PHYTOCHROME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12 ARAGGGCGGGGIEGPT 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40 SRAGGGGGGGGGGT 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PF00989; PAS; 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            372 37
1178 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                               SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00512;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RU17_MOUSE
Q62376;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BINDING
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SNRP70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RU17_MOUSE
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                                                                                                                             Hornig H., Fischer U., Costas M., Rauh A., Luehrmann R.; Analysis of genomic clones of the murine UIRNA-associated 70-kba protein reveals a high evolutionary conservation of the protein between human and mouse."; Lachem. 182.75-50(1989).

Eur. J. Blochem. 182.15-50(1989).

I. REGION OF UI-SNRNA. THE TRUNCATED ISOFORM CANNOT BIND UI-SNRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nuclear protein; Ribonucleoprotein; RNA-binding; Phosphorylation; Alternative splicing.
                                                                                                                                                                                                                                                                                          -!- PTM: EXTENSIVELY PHOSPHORYLATED ON SERINE RESIDUES IN THE C-TERMINAL REGION (BY SIMILARITY).
                                                                                                                                                                                                                                                           -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND 2; ARE PRODUCED BY ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RU17_HUMAN STANDARD; PRT; 437 AA.
P08621; P78493; Q99377; Q15364; P78494; Q15686; Q15687; Q9UE45;
Q9UE46; QQUE47; Q9UE48; Q15689; Q9UFQ6;
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m
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ARG/ASP/GLU-RICH (MIXED CHARGE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 378;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RNA-BINDING (RRM).
ARG/GLU-RICH (MIXED CHARGE).
POLY-GLY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E669C31BCA365AA0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MISSING (IN ISOFORM 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-AUG-1988 (Rel. 08, Created)
01-AUG-1988 (Rel. 08, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26.1%; Score 51.5; I 44.0%; Pred. No. 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POLY-GLY.
                                                                              SEQUENCE FROM N.A. (ISOFORMS 1 AND 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X15769; CAA33777.1; -.
EMBL; X15770; CAA33777.1; JOINED.
EMBL; X15771; CAA33777.1; JOINED.
EMBL; X15772; CAA33777.1; JOINED.
EMBL; X15774; CAA33777.1; JOINED.
EMBL; X15776; CAA33777.1; JOINED.
EMBL; X15776; CAA33777.1; JOINED.
HSSP; P09651; 1HA1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=89276388; PubMed=2525092;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS50102; RRM; 1. PROSITE; PS00030; RRM_RNP_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            43722 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MGD; MGI:98341; Snrp70.
InterPro; IPR000504; RRM.
Pfam; PF00076; rrm; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11; Conservative
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96
378
                                                                                                                                                                                                                                               SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00360; RRM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            378 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                 NCBI_TaxID=10090;
                                                                                               STRAIN=BALB/C;
                                                                                                                                                                                                                                              (BY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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DOMAIN
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E28855
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NUCLEIC ACIDS RES. 21:2815-2822(1993).
-I- FUNCTION: MEDIATES THE SPLICING OF PRE-MRNA BY BINDING TO THE LOOP
I REGION OF UI-SNRNA. THE TRUNCATED ISOFORMS CANNOT BIND UI-SNRNA.
-I- ALTERNATIVE PRODUCTS: 4 ISOFORMS; 1 (SHOWN HERE), 2, 3 AND 4; ARE
PRODUCED BY ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-91065657; PubMed-2147422; Spritz R.A., Strunk K., Surowy C.S., Mohrenweiser H.W.; Human Ul-70K ribonucleoprotein antigen gene: organization, nucleotide sequence, and mapping to locus 19q13.3."; Genomics 8:371-379(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Northemann W., Berg H., Stahnke G., Walter M., Hunt N., Fenning S.; "Identification of an inhibitory element within the human 68-kDa (UI) ribonucleoprotein antigen. Protein Expr. Purif. 6:748-756(1995).
20-AUG-2001 (Rel. 40, Last annotation update)
UI SMALL NUCLEAR RIBONUCLEOPROTEIN 70 KDA (UI SNRNP 70 KDA) (SNRNP70)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -i- DISEASE: MAJOR RIBONUCLEOPROTEIN ANTIGEN RECOGNIZED BY THE SERA FROM PATIENTS WITH AUTOIMMUNE DISEASES, SUCH AS SYSTEMIC LUPUS ERYTHEMATOSUS.
                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE-87133480; PubMed-3028775;
MEDLINE-87133480: Fixer Senter R., Schneider C., Lottspeich F.,
Argos P., Luhrmann R., Philipson L.;
"Cloning of the human cDNA for the UI RNA-associated 70K protein.";
EMBO J. 5:3209-3217(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query C.C., Bentley R.C., Keene J.D.; a common RNA recognition motif identified within a defined Ul RNA binding domain of the 70K Ul snRNP protein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Francke U.;
The human U1-70K snRNP protein: cDNA cloning, chromosomal
localization, expression, alternative splicing and RNA-binding.";
Nucleic Acids Res. 15:10373-10391(1987).
                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutharia; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -i- PTM: THE N-TERMINUS IS BLOCKED.
-i- PTM: EXTENSIVELY PHOSPHORYLATED ON SERINE RESIDUES IN THE C-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      phosphorylates arginine/serine rich domains typical of splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Poustka A., Klein M., Mewes H.-W., Gassenhuber J., Wiemann S.;
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'Identification of an snRNP-associated kinase activity that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=93324364; PubMed=8332490;
Woppmann A., Will C.L., Kornstaedt U., Zuo P., Manley J.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Spritz R.A., Strunk K., Surowy C.S., Hoch S.O., Barton D.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORM 1), AND RNA-BINDING DOMAIN MEDLINE-89195226; PubMed-2467746;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING. MEDLINE-88096573; PubMed-2447561;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 219-348, AND PHOSPHORYLATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Liver;
MEDLINE=96363460; PubMed=8746626;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORM 4).
                                                                                                                     SNRP70 OR RPU1 OR UIAP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cell 57:89-101(1989).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EVYGPTKRIHWYSKRSGKPRGYAFIEYEHFRDMHS -> M
EVALHRFGRGLYWLGYWARLSVGRYRRYRDGDTGRGFCRAGP
VLTRGPSGDSSPLPLPTSVTA (IN ISOFORM 4).
166 AYKHADG -> TTQLACS (IN ISOFORM 3).
ANTRADG -> TTQLACS (IN ISOFORM 3).
ANTRADG (IN ISOFORM 3).
231 MISSING (IN ISOFORM 2).
51556 MW; F1020BFSC40CF97D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APYIREFEDPRDAPPPTRAETREERMERKRREKIERRQGEV
ETELKMWDPHNDPNAQGDAFKTLFVARVNYDTTESKLRREF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000504; RRM.
Pfam; PF00076; rrm; 1.
SMART; SM00360; RRM; 1.
PROSITE; PS00030; RRM, 1.
PROSITE; PS00030; RRM_RNP_1; 1.
Nuclear protein; Ribonucleoprotein; RNA-binding; mRNA processing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 437;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Phosphorylation; Alternative splicing.

DOMAIN 103 181 RNA-BINDING (RRM).

DOMAIN 231 310 ARG/GLU-RICH (MIXED CHARGE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 51.5; I
Pred. No. 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POLY-GLY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POLY-GLY
                                                                                                                                             CAA29964.1; ALT_INIT.
CAA29966.1; ALT_INIT.
CAA30304.1; -.
                                                                                                             EMBL; X04654; CAA28352.1; ALT_INIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAA36571.1; JOINED.
AAA36571.1; JOINED.
AAA36571.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                 JOINED.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAA36571.1; -. AAA36571.1; JOINED.
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44.08;
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AAA36572.1;
AAA36572.1;
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                                                                                                                                                                                                                  CAA29965.1;
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AAA36573.1;
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AAA36572.1;
AAA36573.1;
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CAA29960.1
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HSSP; P09651; 1UP1.
MIM; 180740; -.
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167
223
437 AA;
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Best Local Similarity
Matches 11; Conserv
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                                                                                                                                                      x06815;
                                                                                                                                                                                                 X07402;
                                                                                                                                                                                                                  X06816;
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                                                                                                                                   X06814;
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RESULT 44 FXGA\_CHICK

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181 GRIVKGWRPRRLGGGLGGTRRGGAD 205

3 GPTLRQWLAARAGGGCGG---GGIE 24

01-MAR-1989 (Rel. 10, Created) 01-MAR-1989 (Rel. 10, Last sequence update) 20-AUG-2001 (Rel. 40, Last annotation update) Ul SMALL NUCLEAR RIBONUCLEOPROTEIN 70 KDA (UI SNRNP 70 KDA) (SNRNP70)

471 AA

PRT;

STANDARD;

RU17\_XENLA P09406;

RU17\_XENLA

Būkaryota; Metažoa; Chordata; Craniata; Vertebrata; Buteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;

Xenopus laevis (African clawed frog).

(U).-70K)

Xenopodinae; Xenopus.

SEQUENCE FROM N.A. NCBI\_TaxID=8355

Philipson L.;

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                                                                                                                                                                                                                                                                                                                                                                                                                               THEIR TARGET GENES.
SUBCELULAR LOCATION. NUCLEAR (POTENTIAL).
TISSUE SPECIFICITY: RETINA.
TISSUE SPECIFICITY: RETINA.
TISSUE SPECIFICITY: RETINA.
BEVELOPMENTAL STAGE: CAN BE DETECTED IN REGIONS INCLUDING
PRIMORDIAL RETINA AND NEUROEPITHELIUM BY EMBRYONIC DAY 2 (82). AT
BENTHELIUM AS WELL AS IN PART OF THE DIENCEPHALON, AND AT ST IS
EXPRESSED IN RETINAL AS IN PART OF THE DIENCEPHALON, AND AT ST IS
EXPRESSED IN RETINAL ANGLINON CELLS. LEVELS BEGIN TO DECLINE FROM
                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                 15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
FORKHEAD PROTEIN GLA (FORKHEAD-RELATED PROTEIN FKHL2) (TRANSCRIPTION FOXCRA OR FKHL2 OR HPHBF2.
                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: MAY DETERMINE THE NASCTEMPORAL AXIS OF THE RETINA, AND CONSEQUENTLY SPECIFY THE TOPOGRAPHICAL PROJECTION OF THE RETINAL GANGLION-CELL AXONS TO THE TECTUM BY CONTROLLING EXPRESSION OF
                                                                                                                                                                                                                                                                                                         Yuasa J., Hirano S., Yamagata M., Noda M.;
"Visual projection map specified by topographic expression of
transcription factors in the retina.";
Nature 382:632-635(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 51.5; DB 1; Length 440;
Pred. No. 76;
0; Mismatches 5; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00657; FORK_HEAD_1; 1.
PROSITE; PS00658; FORK_HEAD_2; 1.
PROSITE; PS50039; FORK_HEAD_3; 1.
Transcription requiation; DNA-binding; Nuclear protein;
Developmental protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POLY-PRO.
82266C2E1E103A48 CRC64;
     440 AA.
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FORK-HEAD.
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                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. STRAIN-WHITE LEGHORN; TISSUE-Retina;
                                                                                                                                                                                                                                                                                   MEDLINE=96338226; PubMed=8757134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001766; Fork_head.
Pfam: PF00250; Fork_head; 1.
PRIWTS; PR00053; FORKHEAD.
SMART; SM00339; FF; 1.
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   STANDARD;
                                                                                                                                             Gallus gallus (Chicken)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  440 AA;
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                                                                                                                                                                                                                    NCBI_TaxID=9031;
   FXGA_CHICK
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(U1 70K).";
EMBO J. 7:4311-4321(1988).
-!\* FUNCTION: MEDIATES THE SPLICING OF PRE-MRNA BY BINDING TO THE STEM
LOOP I REGION OF UI-SNRNA.

-! - SIMILARITY: CONTAINS 1 RNA RECOGNITION MOTIF (RRM).

"Structure and expression of a Xenopus gene encoding an snRNP protein

MEDLINE-89210819; PubMed-2468488; Etzerodt M., Vignali R., Scherly D., Mattaj I.W., Ciliberto G.,

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between the Swiss Institute of Bioinformatics and the EMBL outstation. The European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration
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PROSITE; PS00030; RRM_RNP_1; 1.
Nuclear protein; Ribonucleoprotein; RNA-binding; mRNA processing.
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ARG/ABLO-RICH (MIXED CHARGE).
ARG/ASP/GLD-RICH (MIXED CHARGE).
959A8BB31064C3FC3
CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26.1%; Score 51.5; DB 1; Length 471; 44.0%; Pred. No. 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8; Indels
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HSSP; P09651; 1UP1.
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Pfam; PF00076; rrm; 1.
SMART; SM00360; RRM; 1.
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Gaps

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Conservative

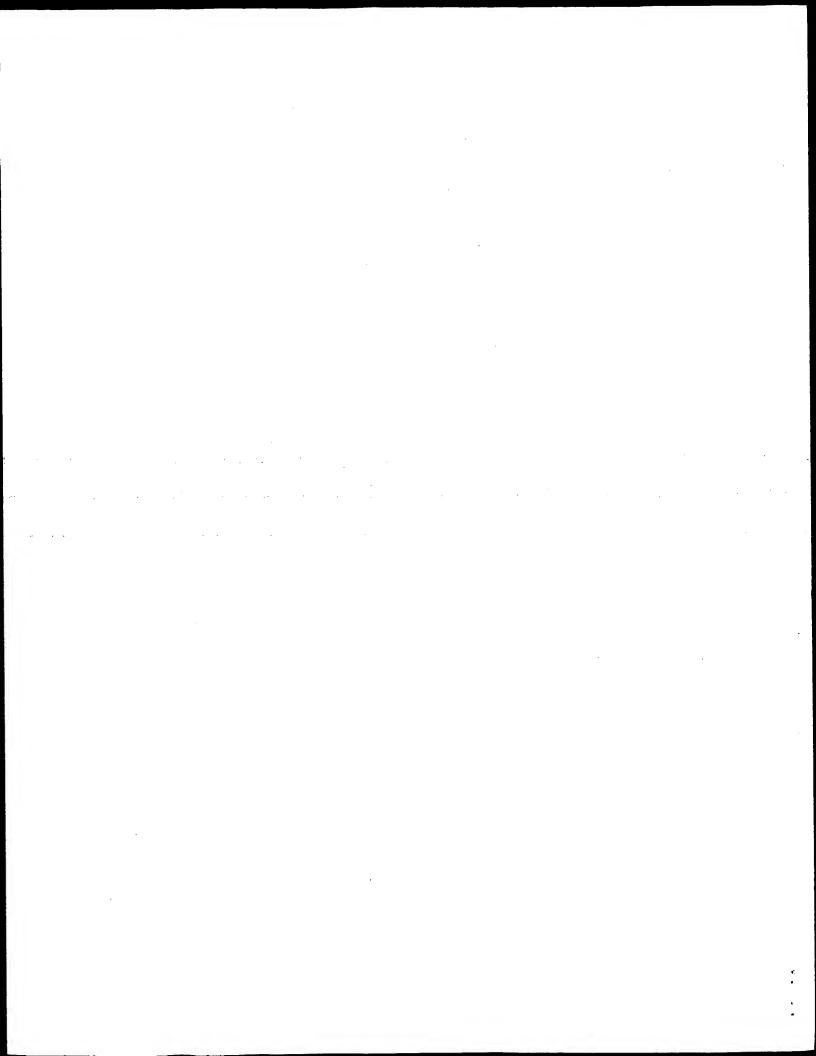
12;

Matches

105 GP---QKAAAAGGGGAGGGG 121

3 GPTLRQWLAARAGGGCGGGG 22

á q



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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

December 26, 2001, 10:27:23 ; Search time 22.51 Seconds (without alignments) 233.932 Million cell updates/sec

US-09-422-838C-33

1 IEGPTLROWLAARAGGGCGGGGTEGPTLROWLAARA 36 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

473505 segs, 146272329 residues Searched:

473505 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 100 summaries

SPTREMBL\_17:\* Database :

sp\_virus:\*
sp\_vertebrate:\*
sp\_unclassified:\* sp\_invertebrate:\* sp\_organelle:\* sp\_phage:\* sp\_archea:\*
sp\_bacteria:\*
sp\_fungi:\*
sp\_human:\* sp\_rodent:\* sp\_plant:\* sp\_mammal:\* sp\_mhc:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	O54108 streptomyce	O91qc9 orvza sativ	Ogova9 coturnix co	Office oryga sativ	O9sdk6 orvza sativ	Ogueal homo sapien	Ogunw9 homos aprien		_	_	_				049843 mycobacteri	O91wc8 orvza sativ	035392 mis misculu	O83436 trenonema n	09hea4 neurospora
SUMMARIES	ID	054108	63760	3 Q9PVG9	0 Q9FTZ5	0 09SDK6	Q9UEA1	6MND60	043267	019476	O9VBC7	Q9UAE7	014060	03000	O9AD76	049843	O9LWC8	035392	083436	09неа4
	Query Match Length DB	865 2	360 10	431 13	202 10	439 10	464 4	492 4	498 4	500 5	654 5	654 5	454 4	488 2	496 2	518 2	125 10	492 11	683 2	801 3
dР	Query	34.0	33.0	32.7	31.2	31.0	30.5	30.5	30.5	30.5	30.5	30.5	30.2	30.2	30.2	30.2	29.9	29.9	29.9	29.9
	Score	29	65	64.5	61.5	61	9	9	9	9	9	9	59.5	59.5	59.5	59.5	59	59	59	59
	Result No.	-	7	m	4	2	ø	7	ω	6	10	11	12	13	14	15	16	17	18	19

homo sapien mesocricet oryza sati thermus aqu thorsophila trichoderma zea mays	mus musc myxococcu mycobacte arabidop petromyz metarhizi home aspi oryza sa polyangiu homo sapi homo sapi	aeropyrum oryza sa homo sapi homo sapi bacillus bacteriop caenorhab arabidop oryza sa anolis c drosopil phanerochi	homo sapien oryza sati salmonella neurospora arabidopsi arabidopsi caenorhabdi	09epm9 mus musculu 09epm1 mus musculu 09epm1 mus musculu 016560 homo sapien 09ics7 pseudorabie 02cs7 pseudorabie 02cs7 pseudorabie 02bse2 homo sapien 0210b6 streptonyce 02917 drosophila 02966m8 drosophila 0296m8 drosophila 029641 drosophila 0296116 oryza sativ 02941 drosophila 0296116 oryza sativ 02941 drosophila 029691 catharanthu 029290 drosophila 02925 droso
70 0	- 0	0 00%		11 Q9EPM9 4 Q16560 12 Q9ICS7 Q9ZRB9 Q9ZRB9 Q9ZRB9 Q9LB5 Q9L086 5 Q9NGF7 5 Q9NGF7 5 Q9NGF1 10 Q9NL16 5 Q9WAF1 10 Q9KRA1 10 Q9KRS9 10 Q9KRS9 11 Q6SIRS 2 Q5SIRS 4 Q9BYD8
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RESULT
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                   O9sxi9 oryza sativ
O9v410 drosophila
O9vyu0 drosophila
O30914 streptomyce
                                                                                                 Q9z3x4 ralstonia s
Q9cxs4 mus musculu
Q9z0t7 rattus norv
29vbw6 drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Frain-A3(2);

MEDLINE-97000315;

PubMed=8843436;

Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J.,

Kinashi H., Hopwood D.A.;

Kinashi H., Hopwood D.A.;

Kinashi H., Hopwood D.A.;

A set of ordered cosmids and a detailed genetic and physical map for the B Mb Streptomyces coelicolor A3(2) chromosome.";

Mol. Microbiol. 21:77-96(1996).

Mol. Microbiol. 21:77-96(1996).

EMBL: A.021529; CALAIGA49.1;

InterPro; IPR000130; Zn_WTPeptdse.

InterPro; IPR000150; McOllptase.

Pfam: PF00152; Peptidase_M9; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
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Pred. No. 4.9;
0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Murphy L., Harris D.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      865 AA; 92392 MW; 2145740361275F8F CRC64;
                                                                                                                                                                                                                                                                                                                                                             01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PUTATIVE SECRETED PROTEASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   360 AA.
                                                                                                                                                                                                                                                                                                                     865 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR00931; MICOLLPTASE.
PROSITE; PS50093; PKD; 1.
PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
                                                                                                                                                                                                             ALIGNMENTS
                   Q9SXI9
Q9V410
Q9VYU0
O30914
Q9Z3X4
Q9ZXS4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-2000 (TrEMBLrel. 15, Created)
                                                                                                                                                                                                                                                                                                                       PRT;
  O9VBW6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34.0%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              651 WLAACAAGNCGGGGTNPP 668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 WLAARAGGCGGGGIEGP 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 66.73
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptomyces coelicolor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00089; PKD; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=1902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-A3(2);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=A3(2);
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09LGC9;
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                                                                                                                                                                                                                                                                                                                     054108
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054108
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                        Oryza sativa (Rice).
Sukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17;
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                                                                                                                                                                                                                                                                                                                                  STRAIN=CV. NIPPONBARE;
Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC clone:P0462H08.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 33.0%; Score 65; DB 10; Length 360; Best Local Similarity 52.0%; Pred. No. 3.5; Matches 13; Conservative 2; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL: AP002525: BAB07996.1; -.
InterPro; IPR000571; Zf-CCCH.
Pfam; PF00042; Zf-CCCH; 4.
SMART: SM00356; ZnF_CSH1; 4.
SEQUENCE 360 AA; 37368 MW; 5105598D7E1C77B2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Liu Y., Xue J.X., Zhang W., Fu D.C., He R.Q., Xue Z.G.;
"qBrain-2, a POU-box gene expressed in quail embryos.";
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
-; SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-; SIMILARITY: TO OTHER HOMEOBOX DOMAINS.
EMBL; AF091043; AAF00040.1;
-HSSP; P14859; LOCT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA-binding; Homeobox; Nuclear protein.
SEQUENCE 431 AA; 43722 MW; 1DC47E53F9ACC7D5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
POU-BOX PROTEIN BRAIN-2.
or oun-2001 (TrEMBLrel. 17, Last sequence update) PUTATIVE ZINC FINGER PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Coturnix coturnix japonica (Japanese quail).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     431 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . 26 LEGPMWRMGLGGGGGGGGGGGGDG 50
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PROSITE; PS50071; HOMEOBOX_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001356; Homeobox.
InterPro; IPR000327; POU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00046; homeobox; 1.
Pfam; PF00157; pou; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PKINTS; PR00028; POUDOMAIN.
ProDom; PD000583; POU; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00035; POU_1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00389; HOX; 1.
SMART; SM00352; POU; 1.
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                                                                                                                                                                                                                                                         NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Coturnix.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09PVG9;
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337 YLGAGAGGGAGGG--GPLVAAAAAGA 362
                                          Created)
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                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                            IPR001859; Ribosomal_P2.
                                                                                                                                                                                                                                                                                                                                                                            NON_TER 1 1
SEQUENCE 464 AA; 45901 MW;
                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00456; RIBOSOMALP2.
                                         (TrEMBLrel, 13,
                                                                                                                                                                                                                                                                                                                                      Pfam; PF00013; KH-domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     15; Conservative
                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                SMART; SM00322; KH; 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human)
                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
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                                                                                                                            NCBI_TaxID=9606;
                                         01-MAY-2000
                                                                                                                                                                                                                                                                                                                              InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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                             Q9UEA1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTY ;
                C9UEA1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6MND60
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
   Q9UEA1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09UNW9
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                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                  Eukaryota; Viridipiantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Enhartoideae; Oryzeae; Oryza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oryza sativa (Rice).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-CV. NIPPONBARE;
SASSANT T., Matsumoto T., Yamamoto K.;
Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC clone:P0436E04.";
                                                                                                                                                                                                                                                                                                                                                                          DB 10; Length 202;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=CV. NIPPONBARE;
Sasaki T., Matsumoto T., Yamamoto K.;
"Organ sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31.0%; Score 61; DB 10; Length 439; 32.0%; Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         clone P0705D01.";
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AP000492; BAA84610.1; -. SSQUENCE 439 AA; 47297 MW; 533EEC240CEA1BA2 CRC64;
                                                                                                                                                                                                                                                                                                        Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases. EMBL, AP002818; BAB16319.1; -- SEQUENCE 202 AA; 19763 MW; BFC2520037F8E274 CRC64;
                                                                                                       01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
UNAY-2000 (TrEMBLrel. 13, Last annotation update)
HYPOTHERTCAL PROTEIN.
            -----GGGCGGGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                        1 IEGPTLRQWLAARAGGGCGG-----GGIEGPTLRQWLAA 34
                                                                                                                                                                                                                                                                                                                                                                                                  12;
                                                                                     202 AA
                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 5;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              439 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                         Score 61.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-2000 (TrEMBLrel. 13, Created)
                                                                                                                                                                                                                                                                                                                                                                        31.2%;
38.1%;
                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 38.10,
"when 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                     PRELIMINARY;
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                                                                                                                                                                        Oryza sativa (Rice)
                                                                                                                                                 P0436E04.1 PROTEIN.
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Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                        NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=4530;
8 QWLAARA---
                                                                                                                                                           P0436E04.1
                                                                                  09FTZ5
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Lamerdin J.E., McCready P.M., Skowronski E., Viswanathan V.,
Burkhart-Schultz K.J., Gordon L., Dias J., Ramirez M., Stilwagen S.,
Phan H., Velaszo N., Do L., Regala W., Terry A., Garnes J.,
Danganan L., Erler A., Christensen M., Georgescu A., Avila J, Liu S.,
Attix C., Andreise T., Trankheim M., Amico-Keller G., Coefield J.,
Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Krommiller B.,
Arellano A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A.,
Olsen A.S., Carrano A.V.;
Sequence analysis of a 1.9 Mb region in 19q13.2 between APOE and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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MEDLINE=99007301; PubMed=9789075;

MEDLINE=99007301; PubMed=9789075;

The neuronal RNA-binding protein Nova-2 is implicated as the autoantigen targeted in PoMA patients with dementia.";

Proc. Natl. Acad. Sci. U.S.A. 95:13254-13259(1998).

EMBL, AF083898; AAC72355.1; -.

InterPro: IPR000958; KH.

EMBL, RNO0313; KH-domain; 3.

SEQUENCE 492 AA; 49008 MW; 41B63EAF6899256B CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AC006540; AAD13116.1; -.
InterPro; IPR000958; KH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0B16BAE99C271CC3 CRC64;
                                                                                 (TrEMBLrel. 13, Last sequence update) (TrEMBLrel. 17, Last annotation update)
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
RNA-BINDING PROTEIN NOVA-2.
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464 AA.
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53.6%; Pred. No. 17;
iive 2; Mismatches
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                                                                                                                                            RNA-BINDING PROTEIN NOVA-2 (FRAGMENT).
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NCBI_TaxID=6239;
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Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-20197319; PubMed-10735272;
Ueki K., Ramaswamy S., Billings S.J., Mohrenweiser H.W., Louis D.N.;
"ANOVA, a putative astrocytic RNA binding protein gene that maps to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       chromosome 19q13.3.";
Neurogenetics 1:31-36(1997).
Neurogenetics 1:31-36(1997).

-i- FUNCTION: MAY REGULATE RNA SPLICING OR METABOLISM IN A SPECIFIC SUBSET OF DEVELOPING NEURONS (BY SIMILARITY).

-i- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).

-i- TISSUB SPECIFICITY: BRAIN. EXPRESSION RESTRICTED TO ASTROCYTES.

-i- DISEASE: MAY BE A TARGET ANTIGEN IN ONE OF THE UNDEFINED HUMAN PARANEOPLASTIC SYNDROMES.
                                                                                                                                                                                                                           01-JUN-1998 (T.EMBLrel. 06, Last sequence update)
01-JUN-2001 (T.EMBLrel. 17, Last annotation update)
ASTROCYTIC NOVAL-LIKE RNA-BINDING PROTEIN (NEUROONCOLOGIC VENTRAL
                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-UN - 2001 (TrEMBLrel. 17, Last annotation update)
F15B9.5 PROTEIN.
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Nuclear protein; RNA-binding; Repeat; Antigen.
                                                                                                                                                                   498 AA
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2; Mismatches
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POLY-PRO.
POLY-ALA.
POLY-GLY.
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                                             365 YLGAGAGGGAGGG--GPLVAAAAAGA 390
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                       9 WLAARAGGGCGGGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                            Created)
                                                                                                                                                                   PRT;
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Matches 15; Conservative
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                                                                                                                                                                                                                                                                                          (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
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416
498 AA;
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                                                                                                                                                                                                                                                                                            ANTIGEN 3) (FRA
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01-JUN-1998
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Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
A Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
A Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Galle R.F.,
A Annanatides P.G., Scherer S.E., Richards S., Ashburner M., Henderson S.N.,
S. Stuton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
A Stuton G.G., Wortman J.R., Halzej R.G., Change M., Pfelifer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Change M., Pfelifer B.D.,
RA Bril J.F., Agbayani A., An H.-J., Andrews-Pfannkock C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Bessley E.M.,
Besson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Borkova D., Botchan M.R., Buuck J., Brokstein P., Brottler P.,
RA Gherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
A Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
A Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
A Durbin K.J. Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
A Gode K., Gong F., Gorrell J.H., Gu Z., Gunn P., Harris N.L., Harrey D., Heiman T.J., Hernandez J.R., Hobey M.,
Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibbeywam C.,
Alalali M., Kalush F., Karpen G.H., Re Z., Kennison J.A., Ketchum K.A.,
                                                                                                                                                                                                                      Milson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Boffield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lighthing J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
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Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.,
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
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Eukaryota: Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota: Neoptera; Endopterygota: Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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Pred. No. 19;
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                                                                       Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 368:32-38(1994).
EMBL; Z78013; CAB01420.1; -.
Interpro; IPRO01254; Trypsin.
SEQUENCE 500 AA; 53946 MW; 1416327086FE7CF6 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=94150718; PubMed=7906398;
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Best Local Similarity 52.29
Matches 12, Conservative
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SEQUENCE FROM N.A.
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Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Liasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Liu X., Mattei B., McIntosh T.C., Morledd M.P., Morberson D., Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., Ralazzolo M., Pittman G.S., Panel J., Puri V., Rese M.G., Rainston K., Saunders R.D.C., Scheeler F., Shen H., Shenet K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Spier E., Siden Krämos I., Simpson M., Skropski M.P., Smith T., Spier E., Wardling A.C., Stapleton M., Strong R., Sun E., Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Walliams S.M., Woodage T., Weinstock G.M., Weissenbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q., A., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q., A., A., Myers E.W., Rubin G.M., Venter J.C.; Shin K., Smith H.O., R., Myers E.W., Rubin G.M., Venter J.C.; Smith H.O., R., Myers E.W., Rubin G.M., Venter J.C.; Smith H.O., R., Melsendore sequence of Drosophila melanogaster."; BMEL, AED003757, AAF56615.1; -.
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Siekhaus D.E., Fuller R.S.;
"A role for amontillado, the Drosophila homolog of the neuropeptide precursor processing protease PC2, in triggering hatching behavior.";
U. Neurosci. 19:6942-6954 (1999).
EMBL; AF033117; AAD49105.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 654;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; Irrocallian Pf01483; P. 1.
Pfam; PF01082; Peptidase_S8; 1.
Primys; PF00082; Peptidase_S8; 1.
Probom; PB000717; P_domain; 1.
Probom; PS00137; SUBTILASE_ASP; 1.
PROSTIE; PS00137; SUBTILASE_ASP; 1.
PROSTIE; PS00138; SUBTILASE_BRR; 1.
FROSTIE; PS00138; SUBTILASE_BRR; 1.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PROHORMONE AND NEUROPEPTIDE PROCESSING PROTEASE.
AMON OR PC2 OR CG6438.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  654 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30.5%; Score 60; DB 48.0%; Pred. No. 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                 FIYBase; FBgn0023179; amon.
InterPro; IPR000209; Peptidase_S8.
InterPro; IPR002884; P_domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=99365357; PubMed=10436051;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 LRQWLAARAGGGCG--GGGIEGPTL 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP; P00782; 2SBT.
FlyBase; FBgn0023179; amon.
InterPro; IPR000209; Peptidase_S8.
InterPro; IPR002884; P_domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam: PF01483; P; 1.
Pfam: PF00082; Peptidase_S8; 1.
PRINTS: PR00723; SUBTILISIN.
ProDom; PD000717; P_domain; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9UAE7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9UAE7
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"Coproporabytinogen oxidase: gene organization and description of a
muttation leading to exon 6 skipping.";
Hum. Mol. Genet. 3:1325-1330(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                           ;
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                                                                                                                                                                                                          30.5%; Score 60; DB 5; Length 654;
48.0%; Pred. No. 24;
tive 3; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                    71733 MW; D021D4882293C996 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS01021; COPROGEN_OXIDASE; 1.
SEQUENCE 454 AA; 50152 MW; 6EC3D15FD8FD86B5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11 GPC---WLVARGGGGGPRAWSQCGGGG----LRAW 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             454 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        488 AA.
PROSITE; PS00136; SUBTILASE_ASP; UNKNOWN_1.
PROSITE; PS00137; SUBTILASE_HIS; 1.
PROSITE; PS00138; SUBTILASE_SER; 1.
PPCTOCASE; Neuropeptide.
SEQUENCE 654 AA; 71733 MW; D021D4882293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 30.2%; Score 59.5; D
Best Local Similarity 44.4%; Pred. No. 19;
Matches 16; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001260; Coprogen_oxidas.
Pfam; PF01218; Coprogen_oxidas; 1.
PRINTS; PR00073; COPRGNOXDASE.
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                                                                                                                                                                                                                                                                                                                               6 LRQWLAARAGGGCG -- GGGIEGPTL 28
                                                                                                                                                                                                                                                                                                                                                                 | | | | | | | | | | | | 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=PLACENTA;
MEDLINE=95078835; PubMed=7987309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 101-454 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COPROPORPHYRINGEN OXIDASE.
                                                                                                                                                                                                                                      Best Local Similarity 48.0
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-PLACENTA;
                                                                                                                                                                                                             Query Match
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9; Gaps

Score 59.5; DB 2; Length 496; Pred. No. 21; 3; Mismatches 6; Indels

Query Match 30.2%; Best Local Similarity 43.8%; Matches 14; Conservative 4 PTLRQWL-----AARAGGGCGGGIEGP 26

54E110C4F86231A4 CRC64;

49548 MW;

496 AA;

SEQUENCE

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MEDLINE-21128732; PubMed-11234002;

Cole S.T., Egilmeier K., Parkhill J., James K.D., Thomson N.R.,

Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,

Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,

Davies R.M., Devlin K., Duthoy S., Fellwell T., Fraser A., Hamlin N.,

Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,

Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,

Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,

Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,

Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J., Kinashi H., Hopwood D.A.;
"A set of ordered cosmids and a detailed genetic and physical map for the B Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
EMBL; AL512667; CAC21636.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                Mycobacterium leprae.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30.2%; Score 59.5; DB 2; Length 488; 43.3%; Pred. No. 21; Live 2; Mismatches 8; Indels 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A., Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seeger K.J., Harris D.;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  488 AA; 52800 MW; 188918856F9774AA CRC64;
                (TrEMBLrel. 17, Last sequence update) (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (TrEMBLrel. 17, Last sequence update) (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                      "Massive gene decay in the leprosy bacillus.";
Nature 409:1007-1011(2001).
EMBL; AL589320, CAC31378.1; -.
PRIGPTO: JPR000765; GTP1_0BG.
PRINTS; PR00326; GTP10BG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     496 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 PTLRQW-----LAARAGGGGGGGGIEGP 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PUTATIVE INTEGRAL MEMBRANE PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-97000351; PubMed-8843436;
                             01-JUN-2001 (TrEMBLrel. 17, Last POSSIBLE ATP/GTP-BINDING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 30.2%
Best Local Similarity 43.33
Matches 13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptomyces coelicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Complete proteome. SEQUENCE 488 AA;
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                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                        NCBI_TaxID=1769;
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01-JUN-2001
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                01-JUN-2001
01-JUN-2001
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Q9AD76
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Gaps
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Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1769;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oryza sativa (Rice).
Sukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
clone:P0483F08.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30.2%; Score 59.5; DB 2; Length 518; ilarity 43.3%; Pred. No. 22; Conservative 2; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (MAY 2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AP002094; BAA96216.1; -
SEQUENCE 125 AA; 13396 MW; C609D8D0B07BC505 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases.
EMBL; U00019; AAA17274.1; -.
SEQUENCE 518 AA; 56001 MW; 6641916CC84F374B CRC64;
                                                                                                                                                                                                                                                                         Robison K.;
Submitted (NOV-1993) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                               Submitted (JAN-1994) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
HYPOTHETICAL PROTEIN.
                                                                                                                                   01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      125 AA
                                                                                       518 AA
4 PTLROW-----LAARAGGGCGGGGIEGP 26
                                                                                                                   01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last seq
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                                                                                       PRT;
                                                                                       PRELIMINARY;
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                                                                                                                                                                                 Mycobacterium leprae.
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Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                   Smith D.R.;
                                                                                                                                                                                                                                                                                                                                                                                                Robison K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                       049843;
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Complete genome sequence of Treponema pallidum, the syphilis
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                                                                                                                                                                                                                               Pfam; PF01436; NHL; 4.
Pfam; PF00515; TPR; 1.
                                                                                                                                                                                                                                                                                                                                     683 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Neurospora crassa.
                                                                                                                                                                                                                                                                                                        Complete proteome
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                                                 spirochete.
                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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                RT RT L DR L DR SO SO
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                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-MESENCHYME;
Wu S.C.-Y., Grindley J., Winnier G.E., Hargett L., Hogan B.L.H.;
Mech. Dev. 0:0-0(1997).
EMBL; AF023915; AAB81275.1; -.
                                                                           14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
29.9%; Score 59; DB 10; Length 125; 40.5%; Pred. No. 6.1; tive 2; Mismatches 9; Indels :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29.9%; Score 59; DB 11; Length 492; 70.6%; Pred. No. 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPACE STATES SERVICED STATES STATES STATES SERVICED STATES SERVICED STATES SERVICED STATES SERVICED SE
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                                                                                                                                                                       (TrEMBLrel. 05, Last sequence update)
(TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CONSERVED HYPOTHETICAL PROTEIN.
                                                                                                                             EGPTLRQWLAARA-------GGGCGGGGIEGPTLRQ 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5,
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                                                                                                                                                                                                                                                                                                                                                         492
                                                                                                                                                                                                                                                                                                                                                                             01-JAN-1998 (TrEMBLrel. 05, Created)
                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=NICHOLS;
MEDLINE=98332770; PubMed=9665876;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MESODERM/MESENCHYME FORK HEAD 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRANGFAC; T02492;
MGD; MGI:134741; Foxd2.
InterPro; IPR001766; Fork_head.
Pfam: PF00250; Fork_head; I.
PRINTS; PR00053; FORKHEAD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              384 LROGLKTDAGGGAGGGG 400
                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 LROWLAARAGGGCGGGG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 70.6 tes 12; Conservative
                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00339; FH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q63245; 2HFH.
                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Treponema pallidum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FOXD2 OR MF2.
                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JAN-1998
01-JUN-2001
                                                              17;
Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        083436
083436;
                                                                                                                                                                                                                                                                                                                                                  035392
                                                                                                                                                                                                                                                                                       RESULT 17
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                                                                 Matches
                                                                                                                                                                                                                                                                                                                     035392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           083436
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                           4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariales; Sordariaceae; Neurospora.
                                                                                                                                                                                                                                                                    29.9%; Score 59; DB 2; Length 683; 43.8%; Pred. No. 33; ive 2; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29.9%; Score 59; DB 3; Length 801; 53.8%; Pred. No. 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               German Neurospora genome project;
German Neurospora genome project;
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AL451109; CAC18654.1;
Interpro; IPRO00719; Euk_pkinase.
Interpro; IPRO00719; Euk_pkinase.
Interpro; IPRO002290; Ser_thr_kin_actsite.
SMART; SM00220; STRC; 1.
PROSITE; PSS5011; PROTEN.KINASE_DOM; 1.
APP-binding; Transferase.
SEQUENCE 801 AA; 85468 MW; IBEF5008A0044A33 CRC64;
                                                                                                                                                                                                  74518 MW; F91407FA7094AAD1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2001 (TremBLrel. 16, Last sequence update) 01.JUN-2001 (TremBLrel. 17, Last annotation update) CONSERVED HYPOTHETICAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
01554E13.1 (PEREGRIN (BR140 PROTEIN)) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          801 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 39;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                          7.4 PLILEWL----GNAYYRSGIEGAALHOWGAAR 101
                                                                                                                                                                                                                                                                                                                                                                   ....4 PTLRQWLAARAGGGGGGGGGGTEGPTLRQWLAAR 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        805 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2001 (TrEMBLrel. 16, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            703 GGGGGGGVVDDDGEPDFAGWLAAQA 728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15 GGCGGGGI---EG-PTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
Science 281:375-388(1998).
EMBL; AE001220; AAC65409.1;
TIGR; TP0421;
                                                                                                                                                                                                                                                              Ouery Match 29.99
Best Local Similarity 43.89
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match
Best Local Similarity 53.88
Matches 14; Conservative
                                                                         InterPro; IPR001258; NHL
InterPro; IPR001440; TPR
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PRELIMINARY;
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               P0671B11.11.
Oryza sativa (Rice).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CG13807.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          056434;
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                     Ωp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yamanoto K., Inoue N., Fujimori A., Saito T., Shinkal H., Sakiyama H.;
"Mesocricetus auratus mRNA for type XVII collagen.";
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AB027759; BAA94381.1;
InterPro; IPR000087; Collagen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                э;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match

29.7%; Score 58.5; DB 4; Length 805;
Best Local Similarity 48.1%; Pred. No. 45;
Matches 13; Conservative 3; Mismatches 8; Indels
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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SEQUENCE 1431 AA; 144579 MW; 4315631FEB2C9A5C CRC64;
                                                                                                                                 Palmer S.;
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; Z84485; CAB06488.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   805 805 805 805 805 80851 MW; E28C017F5C545334 CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
COLLAGEN TYPE XVII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
29.7%; Score 58.5; DB 11;
Best Local Similarity 60.0%; Pred. No. 80;
Matches 15; Conservative 0; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 117 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT; 1431 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mesocricetus auratus (Golden hamster).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 QW-LAARAGGG--CGGGGIEGPTLRQW 31
                                                                                                                                                                                                                                                                                                   Pfam; PF00439; bromodomain; 1.
Pfam; PF00658; PHD; 1.
Pfam; PF00655; PWP; 1.
PRINTS; PR00503; BROMODOMAIN.
PROSITE; PS50014; BROMODOMAIN_2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          438 ARGGGGGGGGGGGT---WGAAPA 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12 ARAGGGCGGGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                               InterPro; IPR000313; PWWP.
InterPro; IPR001487; Bromodomain.
InterPro; IPR001965; PHD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (TrEMBLrel. 16, 17 (TrEMBLrel. 16, 17 (TrEMBLrel. 16, 18)
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00297; BROMO; 1.
SMART; SM00249; PHD; 2.
SMART; SM00293; PWWP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2001 (TrEMBLr P0671B11.11 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10036;
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01-MAR-2001
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NON_TER
SEQUENCE
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Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6; Indels 10; Gaps
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=94124036; PubMed=8294036;
Heinrich T., Erdmann V.A., Hartmann R.K.;
"Sequence of the gene encoding ribosomal protein L11 from Thermus
thermophilus HB8.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12;
                                                                                                                                    [1]
SEQUENCE FROM N.A.
SEQUENCE TON MIPPONBARE;
Sasaki T., Matsumoto T., Yamamoto K.;
Sasaki T., Matsumoto T., PAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thermus aquaticus (subsp. thermophilus).
Bacteria: Thermus/Deinococcus group; Thermus group; Thermus.
NCBI_TaxID=274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 29.4%; Score 58; DB 10; Length 117; Best Local Similarity 41.9%; Pred. No. 7.5; Matches 13; Conservative 2; Mismatches 6; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5; Indels
                                                                                                                                                                                                                                                                                          clone:P0671B11.";
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AP002746; BAB12695.1; -
SEQUENCE 117 AA; 12397 MW; A04617B3DEF9F4B3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NON_TER 1 1 1
SEQUENCE 134 AA; 14336 MW; C8EB750B75EFFC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UTU-2001 (TrEMBLrel. 17, Last annotation update)
CG13807 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29.4%; Score 58; DB 2; 34.4%; Pred. No. 8.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             134 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     170 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94 GCGGGGRGCLSTASVTGPSWRRWTPTRS 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17 GCGGGG-----IEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8 QWLAARAGGGCGGG-----IEGPTL 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36 RWLFARATAGCGSQGDDQKKTPEIEVVGPTL 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1996 (TrEMBLrel. 01, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RIBOSOMAL PROTEIN L11 (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gene 136:373-374(1993).
EMBL; L10371; AAA27503.1; -.
Ribosomal protein.
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Best Local Similarity 34.4%
Matches 11; Conservative
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RX STRAIN=REREEELERY;
RANGIAMERELERY;
RANGIAMER R.A., Lewist S.E., Holt R.A., Evans C.A., Goccyne J.D.,
RANGIAMER, C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RANGIAMER, Basu A., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RANGIAMER, Basu A., Baxendale J., Baraktaroglu L., Beasley E.M.,
RANGIAMER, Basu A., Baxendale J., Baraktaroglu L., Beasley E.M.,
RANGIAMER, Canlam M.R., Bouck J., Baraktaroglu L., Beasley E.M.,
RANGIAMER, Canlam D.A., Bullke C., Davenport L., B., Daviss P.,
RANGIAMER, Canlam D.A., Miller H., Cadieu E., Center A., Chandra I.,
RANGIAMER, Canlam D.A., Miller H., Cadieu E., Center A., Chandra I.,
RANGIAMER, C., Gabrielian A.E., Gary N.S., Gelbart W.M., Glasser R.,
ROOSON K., Gabrielian A.E., Gary N.S., Gelbart W.M., Glasser R.,
RANGIAMER, G., Gabrielian A.E., Gary N.S., Gelbart W.M., Glasser R.,
RANGIAMER, M., Ralush R., Rayepen G. H., Revitz S., Wulp D., Lai Z.,
RANGIAMER, R., Kodirac C.D., Kraft C., Kraft C., Kraft C., Kraft C., Morris S., Molpherson D.L.,
RANGIAMER, R., Kodirac C.D., Kraft C., Kraft C., Morris S., Molpherson D.L.,
RANGIAMER, R., Kodirac C.D., Kraft C., Kraft C., Morris S., Mosherson D.,
RANGIAMER, R., Mixon K.A., Nixon K., Nixon D.M., Nelson D.L.,
RANGIAMER, M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RANGIAMER, R., Mixon K.A., Nixon K., Nixon S., Pan S., Pollard J., Weissenbach J.,
RANGIAMER, R., Tector C., Turner R., Ventra S., Robeler F., Shen H.
Spier E., Spradling A.C., Stapleton M., Stupski M.P., Wasserman D.A., Wasserman D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ij
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Trichoderma reesei (Hypocrea jecorina).
Bukaryota: Kungi, Ascomycota; Perizomycotina; Sordariomycetes;
Hypocreales: Hypocreaceae; Hypocrea.
NCBL_TaxID=51453;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19099 MW; 477D79D55ADF4CE5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2001 (TrEMBLrel. 17, Last annotation update) ACETYLXYLAN ESTERASE PRECURSOR (EC 3.1.1.72).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TremBirel. 01, Created)
(TremBirel. 01, Last sequence update)
(TremBirel. 17, Last annotation update
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 58; DB 5;
Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                302 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 EGPTLRQWLAARAGGGCGGGGIEG 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FlyBase; FBgn0035323; CG13807.
InterPro; IPR002952; Eggshell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 29.4%;
Best Local Similarity 45.8%;
Matches 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         170 AA;
                                        SEQUENCE FROM N.A.
    NCBI_TaxID=7227;
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01-JUN-2001
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                                        Margolles-clark E., Tenkanen M., Soederlund H., Penttilae M.; "Acetyl xylan esterase from Trichoderma reesei contains an active-site serine residue and a cellulose-binding domain."; Eur. J. Blochem. 237:553-560(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -i- PTM: GLYCOSYLATED.
-!- MASS SPECTROMETRY: MW=21806; METHOD=MALDI.
-!- SIMILARITY: CONTAINS 1 FUNGAL-TYPE CELLULOSE-BINDING DOMAIN (CBD).
                                                                                                                                             Poutanen K., Sundberg M., Korte H., Puls J.; "Deacetylation of xylans by acetyl esterases of Trichoderma reesei."; Appl. Microbiol. Biotechnol. 33:506-510(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                        Hakulinen N., Tenkanen M., Rouvinen J.;
"Crystallization and preliminary X-ray diffraction studies of the catalytic core of acetyl Xylan esterase from Trichoderma reesei.";
Acta Crystallogr. D 54.430-432(1998).
-!- FUNCTION: DEGRADEDS ACETYLATED XYLANS BY CLEAVING ACETYL SIDE GROUPS FROM THE HETERO-XYLAN BACKBONE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 OLIGOSACCHARIDES.
-!- ENZYME REGULATION: INHIBITED BY PHENYLMETHYLSULFONYL FLOURIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PFam: PF00734; CBD_1; 1.
Prodom, PD001821; CBD_fungal; 1.
SMART: SM00235; fCBD_FUNGAL; FALSE_NEG.
PROSITE; PS00562; CBD_FUNGAL; FALSE_NEG.
CCALULIOSE GGGTAGATION; HYdrolase; Serine esterase; Glycoprotein; 3D-structure; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LINKER (BY SIMILARITY).
CELLULOSE-BINDING (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (PROBABLE)
SEQUENCE FROM N.A., SEQUENCE OF 158-186, AND CHARACTERIZATION.
                                                                                                                                                                                                                                     Sundberg M., Poutanen K.; "Eurification and properties of two acetylxylan esterases of Trichoderma reesei.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 3; Length 302
                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- CATALYTIC ACTIVITY: DEACETYLATION OF XYLANS AND XYLO-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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BY SIMILARITY.
N-LINKED (GLCNAC. . .) (PI
; BB6EDCA2971A9F2A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
ACETYLXYLAN ESTERASE.
LINKER (BY SIMILARITY
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8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 GPTLRQWLAARAGGGCGGGGIEGPT-----LRQW 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY.
                                                                                                                                                                                                                                                                                  Biotechnol. Appl. Biochem. 13:1-11(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -i- PATHWAY: XYLAN DEGRADATION.
-i- SUBUNIT: MONOMER.
-i- SUBCELLULAR LOCATION: EXTRACELLULAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29.4%; Score 58; 35.9%; Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
                                                                                                                                                                                                                                                                                                              X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BLOCKED
                          MEDLINE=96235218; PubMed=8647098;
                                                                                                                                                                                                                                                                                                                                MEDLINE=98437545; PubMed=9761918;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000254; CBD_fungal.
InterPro; IPR000734; Lipase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30754 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; Z69256; CAA93247.1; -. HSSP; P00725; 2CBH.
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Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31
302
266
302
32
32
121
121
291
301
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                                                                                                                                                                                                          CHARACTERIZATION.
                                                                                                                                  STRAIN-RUIC-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  244
                 STRAIN=RUTC-30;
                                                                                                                                                                                                                          STRAIN-RUTC-30;
                                                                                                                    FUNCTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
MOD_RES
ACT_SITE
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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RESULT Q9XEJ0

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SEQUENCE-21085660; PubMed=11217851;

Kawai J., Shinaqawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Arawai J., Shinaqawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

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Anawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Saito T., Okazaki Y., Golbori T., Bono H., Balalov S., Casavant T.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Ruchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washlo T.,

Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washlo T.,

Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

Lyons P., Marchlonni L., Mashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Sasaki H., Sato K., Schoenbach C., Schoenbach C., Sultaki S.,

Nordone P., Storch K., Full M., Weitz C., Whittaker C., Wilming L.,

Mynshaw-Book S., Woshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Nordone R., Kawai K., Wang K., Rawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                            Enkaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
Panicoldeae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4ayashizaki Y.;
*Punctional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                           Llaca V., Lou A., Young S., Messing J.; "Comparative Analysis of the 22-kDa zein cluster in Z. mays."; Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases. EMBL; AF090447; AADL0310.1; -
                                                                                                                                                                                                                                                                                                                                                                  29.4%; Score 58; DB 10; Length 516; 76.9%; Pred. No. 33; tive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                          Hypothetical protein.
SEQUENCE 516 AA; 48014 MW; 6B40A6043122307A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
6330548622RIK PROTEIN.
                                                01-NOV-1999 (TrEMBLrel. 12, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update) HYPOTHETICAL 48.0 KDA PROTEIN.
                                  01-NOV-1999 (TrEMBLrel. 12, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
   PRT;
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MGD; MGI:1923417; 6330548G22Rik.
InterPro; IPR000504; RRM.
                                                                                                                                                                                                                                                                          InterPro; IPR002952; Eggshell.
PRINTS; PR01228; EGGSHELL.
                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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   PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       359 GGCCGGCCGAT 371
                                                                                                                                                                                                                                                                                                                                                                                                                                   15 GGGGGGGIEGPT 27
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Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                   Zea mays (Maize).
                                                                                                                                                              NCBI_TaxID-4577;
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                Q9XEJO:
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MEDINE=9828987; PubMed=9634230;
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kimura Y., Takashima Y., Tokumasu Y., Sato M.;
Kimura Y., Takashima Y., Tokumasu Y., Cato M.;
"Molecular cloning, sequence analysis, and characterization of a penicillin-resistant DD-carboxypeptidase of Myxococcus xanthus.";
U. Bacteriol. 181:4696-4699(1999).
EMBL; AB023893; BAA83081.1; -.
HSSP; P00733; 1LBU.
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                                                                                                                                  Score 57.5; DB 11; Length 244; Pred. No. 18;
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Pred. No. 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; delta subdivision; Myxobacteria; Myxococcales; Cystobacterineae; Myxococcaceae; Myxococcus.
NCBI_TaxID=34;
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            PROSITE; PS50102; RRM; 1.
PROSITE; PS00030; RRM_RNP_1; UNKNOWN_1.
SROUENCE 244 AA; 29290 MW; 1625D74743CE1245 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-0AN-1998 (TrEMBLrel. 05, Created)
01-0AN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
HYPOTHETICAL 53.3 KDA PROTEIN.
HFLX OR RV2725C OR MTCY154.05C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PENICILLIN-RESISTANT DD-CARBOXYPEPTIDASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8;
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                                                                                                                                                                                                                                                                                                                                                                                                                       302 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Mismatches
                                                                                                                                                                                             2; Mismatches
                                                                                                                                                                                                                                                                                              131 TLRGWIPRRLGGGLGGKKESGQLRFGGRDRP 161
                                                                                                                                                                                                                                      5 TLROWLAARAGGCGG-----GGIEGP 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 IEGPTLRQWLAARAGGGCGGGGIEGPTLR 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .75 IVGP -- KTWSALNSAGGAGG --- SGPTLR 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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MEDLINE=99350441; Pubmed=10419975;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR002477; PG_binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF01471; PG_binding_1; 2. Pfam; PF02557; VanY; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29.2%;
                                                                                                                                            29.2%;
41.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR003709; Vany.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 48.33
Matches 14; Conservative
                                                                                                                                          Ouery Match 29.2 Best Local Similarity 41.9 Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
SMART; SM00360; RRM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Myxococcus xanthus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Carboxypeptidase.
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033230
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A MEDLINE-21016719; PubMed-11130712;

A Theologia A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,

A Theologia A., Care J.R., Palm C.J., Edwan C.L., Brooks S.Y.,

A White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

A White D., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,

A Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

A Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,

A Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Hulzar L.,

R. Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,

A Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,

R. Lin S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,

In X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,

A Militscher J., Miranda M., Nguyen M., Neoney T., Rowley B.,

R. Sakano H., Salzerg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

R. When H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,

When D., Yu G., Fraser C.M., Voysterg M., Vysotskaia V.S., Walker M.,

R. Veguence and analysis of chromosome I of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ij
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
Oliver S., Osborne J., Ouall M.A., Rajandream M.A., Rogers J.,
Rutter S., Seeger K., Skelton S., Squares S., Sqares R., Sulston J.E.,
Taylor K., Whitehead S., Barrell B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the
complete genome sequence.";
Nature 393:37-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II: Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                    Length 495;
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                                                                                                                                                                                                                                                                                                                                      9; Indels
                                                                                                                                                                                                                   11 protein; Complete proteome.
495 AA; 53327 MW; F82BA93092945121 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               299A412EA9925CB0 CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HYPOTHETICAL 7.9 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                  5;
                                                                                                                                                                                                                                                                                                  DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   76 AA
                                                                                                                                                                                                                                                                                                                                      1; Mismatches
                                                                                                                                                                                                                                                                                                Score 57.5;
Pred. No. 36;
                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                           4 PTLRQW-----LAARAGGGCGGGGIEGP 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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EMBL, AC058785, AAG51509.1, -.

Hypothetical protein.

SEQUENCE 76 AA; 7855 MW; 2'
                                                                                                                                                                            EMBL; Z98209; CAB10901.1; -.
                                                                                                                                                                                                                                                                                                29.2%;
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                                                                                                                                                                                                                                                                                                                                      13; Conservative
                                                                                                                                                                                              Tuberculist; Rv2725c; -.
Hypothetical protein; Con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 28.9
Best Local Similarity 73.3
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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Q9C7W8
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Eukzryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; Clavicipitaceae; mitosporic Clavicipitaceae; Metarhizium.
NCBI_TaxID=92637;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                    Petromyzon marinus (Sea lamprey),
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
Petromyzontiformes; Petromyzontidae; Petromyzon.
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Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AJ293217; CAC07216.1;
InterPro: IPR001579; Chitinase_2.
Fian; PF00734; CBD_1: 1.
Fian; PF00734; CBD_1: 1.
SMART; SM00236; fCBD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 28.9%; Score 57; DB 13; Length 377; Best Local Similarity 44.4%; Pred. No. 32; Matches 12; Conservative 2; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA-binding; Homeobox; Nuclear protein.
SEQUENCE 377 AA; 37998 MW; C2DBC19402D3A172 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    414 AA; 43307 MW; D4CE8945B53CD3AD CRC64;
                                                                                                                 01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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Last annotation update)
                                                               377 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS01095; CHITINASE_18; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01.JUN-2001 (TrEMBLrel. 17, Last annote
FUTATIVE ENDOCHITINASE CH12 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          255 QGYTAASYYGVECGGGGGGGGGGGPYL 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2001 (TrEMBLrel, 16, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Metarhizium anisopliae var. acridum.
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                                                                  PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00027; HOMEOBOX_1; 1. PROSITE; PS50071; HOMEOBOX_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP; P06601; 1FJL.
InterPro; 1PR001356; Homeobox.
Pfam; PF00046; homeobox; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2001 (TrEMBLrel. 16, 01-JUN-2001 (TrEMBLrel. 17,
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STRAIN=FI-985 (ARSEF 324);
                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00389; HOX;
                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=7757;
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SEQUENCE
                                                                                              Q9YHD0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9HFMO;
                                                           09YHD0
RESULT 31
Q9YHD0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9HFM0
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4 PTLRQWLAARAGGGGGGGGEG 25
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                                                                 09L8D4;
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                                                  09L8D4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 36
                          RESULT 35
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                                       Q9L8D4
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                                                                                                                                                                                                                                                                                                                    Zhang F., Kurebayashi S., Jetten A.M.; "Cloning and genomic structure of GLIS2, a novel gene encoding a Glirelated, Kruppel-like protein."; Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.

EMBL: AF325914: AAK00954.1;
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                             Gaps
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Sukaryota, Vitálplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae;
Ehrhartoldeae; Oryzeae; Oryza.
                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
clone:P04556708 ";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28.9%; Score 57; DB 10; Length 529; 63.2%; Pred. No. 44; 1ve 2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 28.9%; Score 57; DB 4; Length 524; Best Local Similarity 53.8%; Pred. No. 44; Matches 14; Conservative 0; Mismatches 12; Indels
 Score 57; DB 3; Length 414; Pred. No. 35;
                            6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AP002901; BAB39414.1; -SEQUENCE 529 AA; 55981 MW; 0A5DA55CDD076D24 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                        524 AA; 55704 MW; 3E2C27243DE5A85E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
P0456F08.14 PROTEIN
                                                                                                                                                                         01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
KRUPPEL-LIKE ZINC FINCER PROTEIN GLIS2.
                                                                                                                                                524 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               529 AA.
                          1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                      377 GGTVPQW-----GQCGGEGYSGPT 395
                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 GPTLRQWLAARAGGGCGGGGIEGPTL 28
                                                     3 GPTLRQWLAARAGGGGGGGGGEGPT 27
 28.9%;
48.0%;
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Query Match
Best Local Similarity 48.09
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 28.9 Best Local Similarity 63.2 Matches 12; Conservative
                                                                                                                                                 PRELIMINARY;
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                                                                                                                                                                                                                                Homo sapiens (Human)
                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
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                                                                                                                                                               09BZE0;
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                                                                                                                                                 Q9BZE0
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                                                                                                                     RESULT 33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Nagase T., Kikuno K., Ishikawa K., Hirosawa M., Ohara O.;
Nagases T., Kikuno K., Ishikawa K., Hirosawa M., Ohara O.;
"Prediction of the coding sequences of unidentified human genes.XVII.The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro.";

EMBL; AB040891; BAA95982.1; -.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96 VDGPALVRWLAAR-----GAPGPLREYEEERERARTAOEARRLWLAA 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28.9%; Score 57; DB 2; Length 607; ilarity 32.0%; Pred. No. 51; Conservative 3; Mismatches 7: Indels
                                                                                                                                                                                                Bactería; Proteobacteria; delta subdivision; Myxobacteria; Myxococcales; Sorangineae; Polyangiaceae; Polyangium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 IEGPTLRQWLAARAGGGCGGGGIEGP------TLRQWLAA 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28.9%; Score 57; DB 4; Length 612; 59.1%; Pred. No. 51;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
                                                     Created)
Last sequence update)
Last annotation update)
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.607 AA
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                                                        01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence
01-JUN-2001 (TrEMBLrel. 17, Last annotatin
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  PRT;
                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=20130945; Pubmed=10662695;
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Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
  PRELIMINARY;
                                                                                                                                                                        Polyangium cellulosum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                          STRAIN-SO CE90;
                                                                                                                                                                                                                                                        NCBI_TaxID=56;
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SEQUENCE
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Q9YDB1;
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                  Q9YDB1
RESULT 39
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Ishikawa K., Nagase T., Suyama M., Miyajima N., Tanaka A., Kotani H.,
Nomura N., Ohara O.;
                                                                                                                                                                                                                                                                             Gaps
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DNA Res. 5:169-176(1998).
EMBL: ABO14600: BAA31675.1;
InterPro: IPR003822; PAH.
Pfam; PF02671; PAH; 3.
                                                                                    Oryza sativa (Rice).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta; Magnoliophyta, Liliopsida, Poales, Poaceae;
Ehrhartoideae, Oryzeae, Oryza.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-CV. NIPPONBARE;
Sasaki T., Matsumoto T., Yamamoto K.;
"Orgas astiva nipponbare(GA3) genomic DNA, chromosome 1, PAC clone:P0706B05.";
                                                                                                                                                                                                                                                       Score 57; DB 10; Length 651;
Pred. No. 55;
2; Mismatches 1; Indels
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Pred. No. 94;
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                                                                                                                                                                                                    Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AP002482; BAA96618.1; -
SEQUENCE 651 AA; 69800 MW; 0308FB36B83B62B0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1130 AA; 129358 MW; B767339317ECC96D CRC64;
                                                          Last sequence update)
Last annotation update)
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                                                Created)
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                           PRT;
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61.1%;
                                              01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15,
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Best Local Similarity 54.2%;
                                                                                                                                                                                                                                                                                                                     418 AASGGGFFCTCGGGGVEG 435
                                                                                                                                                                                                                                                                                                12 ARAGGG----CGGGGIEG 25
                                                                                                                                                                                                                                                                           11; Conservative
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                           PRELIMINARY;
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                                                                              HYPOTHETICAL PROTEIN.
                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                               NCBI_TaxID=4530;
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                          Q9LGW5
                                      O9LGW5
      RESULT 37
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Kawarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y., Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosugi H., Hoiyoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H., Yakamiya M., Masuida S., Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi T., Aoki K.-I., Kubota K., Nakamura Y., Nomura N., Sako Y., Kikuchi H.; Complete genome sequence of an aerobic hyper-thermophilic DNA Res. 6:83-101(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19;
                                                                                                                                                                                                                             Archaea; Crenarchaeota; Desulfurococcales; Desulfurococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-CV. NIPPONBARE;
Sasaki T., Matsunnoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
clone:P0498A12."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Onyza sativa nipponbare(GA3) genomic DNA, chromosome 1, BAC clone:OSJNBa0004B13.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases. EMBL, AP003020; BAB39979.1; -. EMBL; AP003018; BAB39964.1; -. SEQUENCE 243 AA; 26243 MW; 029E9344C20E0EC8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AP000060; BAA79986.1; -. Hypothetical protein; Complete proteome. SEQUENCE 176 AA; 19234 MW; 684D7F476A254457 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
E0498A12.7 PROTEIN (OSJNBA0004B13.18 PROTEIN).
                                                                                  01-NOV-1999 (TrEMBLrel. 12, Last sequence update) U-NAR-2001 (TrEMBLrel. 16, Last annotation update) HYPOTHETICAL 19.2 KDA PROPEIN APE1002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----GGGGIEGPTLRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28.7%; Score 56.5; DB 1; 34.9%; Pred. No. 17; ive 1; Mismatches 8;
176 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-CV. NIPPONBARE;
Sasaki I., Matsumoto T., Yamamoto K.;
                                                          Created)
  PRT;
                                                                                                                                                                                                                                                                                                                                                                    STRAIN=K1;
WEDLINE=99310339; PubMed=10382966;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                  (TrEMBLrel, 12, C
(TrEMBLrel, 12, L
(TrEMBLrel, 16, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 28.7
Best Local Similarity 34.9
Matches 15; Conservative
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 ROWLAARAGGGC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oryza sativa (Rice)
                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                  NCBI_TaxID=56636;
                                                                                                                                                                                                     Aeropyrum pernix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=4530;
                                                     01-NOV-1999
01-NOV-1999
                                                                                                                                                                                                                                                             Aeropyrum.
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us-09-422-838c-33.rspt

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InterPro;
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                                 1;
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                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-20020275; PubMed=10551867;
Zitzer H., Honck H.H., Bachner D., Richter D., Kreienkamp H.J.;
"Somatostatin receptor interacting protein defines a novel family of
multidomain proteins present in human and rodent brain.";
J. Biol. Chem. 274:32997-33001(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

SIGUENCE FROM N.A.

Litzer H., Hoenck H.-H., Richter D., Kreienkamp H.-J.;

"The somatostain receptor interacting protein (SSTRIP) defines a novel family of multidomain postsynaptic density proteins.";

submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AF163302; AAD45121.1; ...

ESSP; P06241; ISHF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                     Homo Sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19;
                                 3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zitzer H., Hoenck H., Baechner D., Richter D., Kreienkamp H.;
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF226728; AA675887.1; -.
InterPro: IPR001478; PDZ.
InterPro: IPR001660; SAM.
SMART: SM00228; PDZ; 1.
SMART: SM00454; SAM: 1.
 Length 243;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 56.5; DB 4; Length 1548;
Pred. No. 1.5e+02;
2; Mismatches 6; Indels 19;
                                                                                                                                                                                                          01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
SOMATOSTATIN RECEPTOR-INTERACTING PROTEIN SPLICE VARIANT B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-UUN-2001 (TrEMBLrel. 17, Last annotation update)
SOMATOSTATIN RECEPTOR INTERACTING PROTEIN SPLICE VARIANT A.
                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Receptor.
SEQUENCE 1548 AA; 158853 MW; 8E5209F785A04D73 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 PTLRQWLAARAGG-------GCGGGGIEGPTLR 29
 DB 10;
                                 9
                                                                                                                                                                            PRT; 1548 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT; 2161 AA
                               3; Mismatches
28.7%; Score 56.5; 47.8%; Pred. No. 23;
                                                                               1 IEGPTLROWLAARAGGGCGGGI 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS50106; PDZ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 28.7
Best Local Similarity 35.7
Matches 15; Conservative
                               11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human)
              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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 Query Match
                                                                                                                                                                           6MAN60
                                                                                                                                                                                             CONYM9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09x566
                                                                                                                                                                                                                                                                           SSTRIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 42
                                                                                                                                             RESULT 41
                                 Matches
                                                                                                                                                               6MAN60
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Runst F., Ogsawara N., Moszer I., Albertini A.M., Alloni G.,
Kunst F., Ogsawara N., Bessleres P., Bolotin A., Borchert S.,
Agwedo V., Bertero M.G., Bessleres P., Bolotin A., Borchert S.,
Borriss R., Boursher L., Brans A., Braun M., Brighell S.C., Bron S.,
Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
Brian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
China S.Y., Glaser P., Goffeu A., Golightly E.J., Grandi G.,
A. Guiseppi G., Guy B.J., Hajech J., Harwood C.R., Henaut A.,
Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M.,
Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
A. Median N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
Noone D., O'Reilly M., Ogsawa K., Ogiwara A., Oudega B., Park S.H.,
Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
Presecan E., Pujic P., Purnelle B., Rochee M., Sadaie Y.,
Sato T., Scanlan E., Schleich S., Schroeter R., Shin B.S., Soldo B.,
Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28.7%; Score 56.5; DB 4; Length 2161; 35.7%; Pred. No. 2.1e+02; ive 2; Mismatches 6; Indels 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2161 AA; 225019 MW; SFEFC969CBE98701 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Paik S.H., Hansen J.N.;
Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
SUBLANCIN 168 PRECURSOR PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----GCGGGGIEGPTLR 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria, Firmicutes, Bacillus/Clostridium group, Facillus/Staphylococcus group, Bacillus.
                                                                                                                                                                                                                                                                                                                 ANK_REPEAT; 3.
ANK_REP_REGION; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=98044033; PubMed=9384377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 PTLRQWLAARAGG-----
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Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                        Pfam, PF00023; ank; 6.
Pfam, PF00595; PDZ; 1.
Pfam, PF00536; SAM; 1.
Pfam; PF00018; SH3; 1.
                                                                                                                                                                               SMART; SM00248; ANK; 3
SMART; SM00228; PDZ; 1
                                                                                                                                                                                                                    SMART; SM00228; PDZ; 1
SMART; SM00454; SAM; 1
interPro; IPR001660;
                                 InterPro; IPR001452;
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                                                                                                                                                                                                                                                                                   SMART; SM00326; SI
PROSITE; PS50088;
                                                                                                                                                                                                                                                                                                                                                     PS50297;
                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS50002;
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SEOUENCE
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PROSITE;
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SEQUENCE FROM N.A
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Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
Tosato V., Uchiyama S., Vandehol M., Vannier F., Vassarotti A.,
Viari A., Wambutt R., Wedler E., Wedler H., Weitzenegger T.,
Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;
"The complete genome sequence of the gram-positive bacterium Bacillus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_FaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                no RNA stage; Tailed phages; Siphoviridae.
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Lazarevic V., Duesterhoeft A., Soldo B., Hilbert H., Mauel C.,
Karamata D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28.4%; Score 56; DB 9; Length 56; 44.0%; Pred. No. 6.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases. EMBL; AF020713; AAC12992.1; -.
                                                                                                                                                                                                                                                                                             Kunst F., Ogasawara N., Yoshikawa H., Danchin A.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
EMBL: AFO14938: AAC65331.1:
                                                                                                                                                                                                                                                                                                                                                                                                                     79EC0BF822F9F4C0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               56 AA; 5982 MW; 79ECOBF822F9F4C0 CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 56; DB 2;
Pred. No. 6.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    163 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 6.2;
3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9 WLAARAGG -- GCGGGGIEGPTLRQW 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30 WLQCASGGTIGCGGGAVACQNYRQF 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9 WLAARAGG - GCGGGGIEGPTLRQW 31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28.4%;
                                                                                                                                                                                                                                                                                                                                             EMBL; AF014938; AAC63531.1;
EMBL; Z99115; CAB14066.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                     5982 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07,
07,
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Best Local Similarity 44.0%
Matches 11; Conservative
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Matches 11; Conservative
                                                                                                                                                                                                    Nature 390:249-256(1997)
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NCBI_TaxID=66797;
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SEQUENCE 5
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Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Benfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
Barsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thherry Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
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EMBL, AF067609; AAC17537.1; --
SEQUENCE 163 AA; 16317 MW; A068D74244200258 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lamar E., Kramer J.;
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
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Pred. No. 18;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Search completed: December 26, 2001, 10:29:14
Job timé: 111 sec
STRAIN=BRISTOL N2;
MEDLINE=94150718; PubMed=7906398;
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75.0%;
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Best Local Similarity 75.0
Matches 12; Conservative
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STRAIN-BRISTOL N2;
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US-09-244-298A-232
US-09-516-704-18
US-09-516-704-18
US-09-516-704-18
US-09-516-704-194
US-09-516-704-194
US-08-76-4640-195
US-08-76-4640-195
US-08-973-225-199
US-08-973-225-199
US-09-244-298A-195
US-09-244-298A-195
US-09-244-298A-210
US-09-244-298A-203
US-08-973-225-198
US-09-16-704-203
US-08-973-225-203
US-08-974-298-694-23
US-08-973-225-203
US-08-974-298-694-23
US-08-973-225-203
US-08-973-225-203
US-08-973-225-2
                                                                             Sequence 231, App Sequence 231, App Sequence 131, App Sequence 131, Appl Sequence 193, Appl Sequence 193, Appl Sequence 193, Appl Sequence 193, Appl Sequence 117, Appl Sequence 117, Appl Sequence 117, Appl Sequence 117, Appl Sequence 118, Appl Sequence 117, Appl Sequence 118, Ap
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64.142 Million cell updates/sec
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                                                                                                                         December 26, 2001, 10:26:03; Search time 12.63 Seconds
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/cgn2_6/ptodata/2/jaa/6A_COWB.pep:*
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/cgn2_6/ptodata/2/jaa/PcTUS_COMB.pep:*
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           GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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US-09-516-704-231

US-08-764-640-133

US-08-97-325-133

US-08-247-228A-193

US-09-244-298A-193

US-09-244-298A-193

US-09-516-704-193

US-09-516-704-193

US-09-516-704-193

US-09-516-704-195

US-09-544-298A-17

US-09-544-298A-17

US-09-244-298A-17

US-09-244-298A-185

US-09-244-298A-185

US-09-516-704-185

US-09-516-704-185

US-08-764-640-186

US-08-764-640-186

US-08-764-640-186

US-08-764-640-194

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5-08-973-225-194
5-08-973-225-220
5-09-244-298A-18
5-09-244-298A-19
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                                                                                                                                                                                                                                                                                                                                       212252 seqs, 22503292 residues
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Maximum Match 100%
Listing first 100 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A TITLE OF INVENTION: RECEPTOR NUMBER OF SEQUENCES: 244
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
ALIGNMENTS
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Balasubramanian, Palaniappan
Wagstrom, Christopher R.
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; OTHER INFORMATION: /product= "Ava"
US-08-764-640-231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/764,640
FILING DATE: 11-DEC-1996
CLASSIFICATION: 514
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                                                                                                Sequence 231, Application US/08764640; Patent No. 5869451; Patent No. 5869451
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Deprince, Randolph B.
Podduturi, Surekha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK328
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-249-1000
INFORMATION FOR SEQ ID NO: 231:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
                                                                                                                                                                                   Dower, William J.
Barrett, Ronald W.
Cwirla, Steven E.
Gates, Christian
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COUNTRY: USA
ZIP: 27709
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                                                                              US-08-764-640-231
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APPLICANT:
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38.8%; Score 76.5; DB 3; Length 25; 40.6%; Pred. No. 0.009;
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TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
TITLE OF INVENTION: RECEPTOR
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APPLICATION NUMBER: US/09/244,298A
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Barrett, Ronald W.
Cwirla, Steven E.
Gates, Christian
Schatz, Peter J.
Balasubramanian, Palaniappan
                                                                                                                                                                                                                                                                                                                                                               STREET: Five Moore Drive, P.O. Box 13398 CITY: Research Triangle Park
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                                      Dower, William J.
Barrett, Ronald W.
Cwirla, Steven E.
Gates, Christian
Schatz, Peter J.
Balasubramanian, Palaniappan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/09/244,298A FILING DATE: 11-DEC-1996 CLASSIFICATION: 514 ATTORNEY/AGENT INFORMATION: NAME: HTublec, Robert T. REGISTRATION NUMBER: 36,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: /product= "Ava"
                                                                                                                                                               Wagstrom, Christopher R.
Hendren, Richard W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 231, Application US/09516704; Patent No. 6251864; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                     Deprince, Randolph B.
Podduturi, Surekha
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INFORMATION FOR SEQ ID NO: 231:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: PK. TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                 Glaxo Wellcome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25 amino acids
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                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 2. CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                               USA
; Patent No. 6121238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: US
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                                        APPLICANT:
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APPLICANT:
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ADDRESSEE: Glaxo Wellcome
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Hendren, Richard W.
Deprince, Randolph B.
Podduturi, Surekha
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/516,704
FILING DATE: Ul-war-2000
CLASSIFICATION: <university control of the control of 
                                                                                                                                                                                                                                                                                            ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schatz, Peter J.
Balasubramanian, Palaniappan
Wagstrom, Christopher R.
Hendren, Richard W.
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TELEPHONE: 919-248-1000
INFORMATION FOR SEG ID NO: 231:
SEQUENCE CHARACTERISTICS:
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Patent No. 5869451
Patent No. 5869451 5837683
                                                                                                                                                                            RECEPTOR
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Podduturi, Surekha
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STRANDEDNESS: <Unknown>
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Barrett, Ronald W.
Cwirla, Steven E.
Gates, Christian
                                                                                                                                                                                                              NUMBER OF SEQUENCES: 244
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ZIP: 27709
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APPLICANT:
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CORRESPONDENCE ADDRESS:
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                                                                                            COMPUTER REABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
    Five Moore Drive, P.O. Box 13398
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Balasubramanian, Palaniappan
Wagstrom, Christopher R.
Hendren, Richard W.
                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/764,640
FILING DATE: 11-DEC-1996
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                    NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3281
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Patent No. 5869451
Patent No. 5869451 5837683
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Podduturi, Surekha
STREET: Five Mouse CITY: Research Triangle Park
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Best Local Similarity 100.0%; Pr
Matches 14; Conservative 0;
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STREET: Five Moore Drive, P.C
CITY: Research Triangle Park
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Barrett, Ronald W.
Cwirla, Steven E.
Gates, Christian
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TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Hrubiec, Robert T.
                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 14 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-764-640-13
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APPLICANT: Dower,
                                                             USA
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                                                          COUNTRY: US
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APPLICANT:
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APPLICANT:
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COUNTY: USA
COUNTY: 127109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COPENATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/973,225A
FILING DATE: 04-Dec-1997
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                                                                                                                37.1%; Score 73; DB 3; Length 14; 100.0%; Pred. No. 0.013; Live 0; Mismatches 0; Indels
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NAME: HILDLEC, RODERT T.
REGIERATION NUMBER: 36, 392
REFERRNCE/DOCKET NUMBER: PK3065USW
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MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 193:
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-08-973-225-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wagstrom, Christopher R. Wrighton, Nicholas C.
                                                                                                                                                                                                                                                                                                                                                            Sequence 193, Application US/08973225A Patent No. 6083913 GENERAL INFORMATION:
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Mattheakis, Larry C.
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ADDRESSEE: Glaxo Wellcome
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TELEPHONE: 919-248-1000
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Barrett, Ronald W.
Cwirla, Steven E.
Duffin, David J.
Gates, Christian
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STRANDEDNESS: <Unknown>
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                                                                                                                Query Match
Best Local Similarity 100.
Matches 14; Conservative
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Wrighton, Nicholas C.
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
THROMBORPOLETIN RECEPPOR
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100.0%; Pred. No. 0.013;
tive 0; Mismatches 0; Indels
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
RAPPLICATION NUMBER: US/08/973,225A
FILING DATE: 04-Dec-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 13, Application US/08973225A
Patent No. 6083913
GENERAL INFORMATION:
APPLICANT: Dower, William J.
Barrett, Ronald W.
Cwirla, Steven E.
Duffil, David J.
Gates, Christian
Haselden, Sherril S.
Mattheakis, Larry C.
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NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
           APPLICATION NUMBER: US/08/764,640 FILING DATE: 11-DEC-1996 CLASSIFICATION: 514
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STRANDEDNESS: <Unknown>
                                                                         ATTORNEY/AGENT INFORMATION:
NAME: HTUDIGC, ROBERT T.
REGISTRATION NUMBER: 36,392
REFRENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 193:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 100.
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-764-640-193
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                                                                                                                                                                                                                                                                               TYPE: amino acid
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TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
                                    APPLICANT: Yin, Qun
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
TITLE OF INVENTION: RECEPTOR
NUMBER OF ENQUENCES: 244
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 73; DB 3; Length 14,
Pred. No. 0.013;
                                                                                                                                                                                                                                                                                       COMPOUTER: IBM PC COMPATIBLE
COMPOUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/244,298A
FILING DATE: 11-DEC-1996
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSES: Glazo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
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100.0%; Pred. No. ...
... 0; Mismatches
                                                                                                                                  ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
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Balasubramanian, Palaniappan
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Patent No. 6251864

GENERAL INFORMATION:
APPLICANT: Dower, William J.
Barrett, Ronald W.
Cwirla, Steven E.
Gates, Christian
                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3281
                                                                                                                                                                                                                COUNTK1.
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Ploppy disk
MEDIUM TYPE: Ploppy disk
Deprince, Randolph B. Podduturi, Surekha
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                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Hrubiec, Robert T.
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ZIP: 27709
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 14 amino acids TYPE: amino acid
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Best Local Similarity 100.
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide
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US-09-516-704-13
  APPLICANT:
                                                                                                                                                                             CITY:
STATE:
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APPLICANT: Podduturi, Surekha
APPLICANT: Yin, Qun
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
TITLE OF INVENTION: RECEPTOR
NUMBER OF SEQUENCES: 244
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: FLORPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/244,298A
FILING DATE: 11-DEC-1996
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37.1%; Score 73; DB 3; Le
100.0%; Pred. No. 0.013;
tive 0; Mismatches 0;
                                                                                                                                                                     Schatz, Peter J.
Balasubramanian, Palaniappan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schatz, Peter J.
Balasubramanian, Palaniappan
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Patent No. 6121238
GENERAL INFORMATION:
APPLICANT: Barrett, Ronald W.
APPLICANT: Gates, Christian
APPLICANT: Schatz, Steven E.
APPLICANT: Schatz, Peter J.
                                                                                                                                                                                                            Wagstrom, Christopher R.
Hendren, Richard W.
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Hendren, Richard W.
                              Sequence 13, Application US/09244298A Patent No. 6121238 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                     : Five Moore Drive, P. Research Triangle Park
                                                                                   APPLICANT: Dower, William J.
APPLICANT: Barrett, Ronald W.
APPLICANT: Cwirla, Steven E.
APPLICANT: Gates, Christian
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NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
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SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
                                                                                                                                                                                                                                                                                                                                                                                       Glaxo Wellcome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 37.1
Best Local Similarity 100.
Matches 14; Conservative
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        US-09-244-298A-13
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APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
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us-09-422-838c-33.rai

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SEQUENCE DESCRIPTION: SEQ ID NO: 193: US-09-516-704-193
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APPLICANT: Balasubramanian, Palaniappan
APPLICANT: Waqstrom. Christon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wagstrom, Christopher R.
Hendren, Richard W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 17, Application US/08764640
Patent No. 5869451
Patent No. 5869451
Patent No. 5869451
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Deprince, Randolph B.
Podduturi, Surekha
Yin, Qun
TELEPHONE: 919-248-1000
                                                                               TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Research Triangle Park
                                                         LENGTH: 14 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Hrubiec, Robert T. REGISTRATION NUMBER: 36,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 17:
                 INFORMATION FOR SEQ ID NO: 193: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Barrett, Ronald W.
Cwirla, Steven E.
Gates, Christian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dower, William J.
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                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS: LENGTH: 15 amino acids
                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-764-640-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                  1 IEGPTLROWLAARA 14
                                                                                                                                                                                                                                                                                                                             1 IEGPTLROWLAARA 14
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APPLICANT:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
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Podduturi, Surekha
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37.1%; Score 73; DB 4; Length 14; 100.0%; Pred. No. 0.013; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Dower, William J.
Barrett, Ronald W.
Cwirla, Steven E.
Gates, Christian
Schatz, Peter J.
Balasubramanian, Palaniappan
                                                                                                                                                                               INFORMATION:

TELECOMMUNICATION:

TELECOMMUNICATION INFORMATION:

TELEPHONE: 919-248-1000

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:

LENGTH: 14 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/516,704
FILING DATE: 01-Mar-2000
CLASSIFICATION: <UNKNOWN>
                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/516,704
FILING DATE: 01-Mar-2000
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: HUBLEC, ROBERT T.
REGISTRATION NUMBER: 36,332
REFERENCE/DOCKET NUMBER: PK3281
                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wagstrom, Christopher R.
Hendren, Richard W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 193, Application US/09516704 Patent No. 6251864 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
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  MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
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Matches 14; Conservative
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37.1%; Score 73; DB 4; Length 14; 100.0%; Pred. No. 0.013; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/764,640
FILING DATE: 11-DEC-1996
CLASSIFICATION: 514
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Five Moore Drive, P.O. Box 13398
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APPLICANT: Yin, Qun
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
TITLE OF INVENTION: RECEPTOR
NUMBER OF SEQUENCES: 244
37.1%; Score 73; DB 2; Length 15; 100.0%; Pred. No. 0.014; ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37.1%; Score 73; DB 2; Length 15; 100.0%; Pred. No. 0.014; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 27709

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FOC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: Glaxo Wellcome
Five Moore Drive, P.O. Box 13398
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Balasubramanian, Palaniappan
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                                                                                                                                                                                                                                                                                                                                                                                                                        Wagstrom, Christopher R.
Hendren, Richard W.
                                                                                                                                                                                                                  Sequence 185, Application US/08764640
Patent No. 5869451
Patent No. 5869451 5837683
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REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3281
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 185:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Deprince, Randolph B.
Podduturi, Surekha
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Barrett, Ronald W.
Cwirla, Steven E.
Gates, Christian
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Query Match 37.1
Best Local Similarity 100.
Matches 14; Conservative
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; MOLECULE TYPE: peptide
US-08-764-640-185
                                                                               1 IEGPTLROWLAARA 14
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Best Local Similarity
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                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: DOWEr,
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                                                                                                                                                                                               US-08-764-640-185
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APPLICANT:
APPLICANT:
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US-08-973-225-17
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Gaps
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Mattheakis, Larry C.
Schatz, Peter J.
Wagstron, Christopher R.
Wrighton, Nicholas C.
TILLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
                                                                                                                                                                                                                     Wagstrom, Christopher R.
Wrighton, Nicholas C.
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
THROMBOPOIETIN RECEPOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37.1%; Score 73; DB 3; Length 15; 100.0%; Pred. No. 0.014; Uve 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                               STREET: Five Moore Drive, P.O. Box 13398
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/973,225A FILING DATE: 04-Dec-1997 ATTORNEY/AGENT INFORMATION:
NAME: HINDIEC, ROBERT T.
REGISTRATION NUMBER: 36,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: PK3065USW TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE DESCRIPTION: SEQ ID NO: 17: US-08-973-225-17
                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Research Triangle Park
                                       APPLICANT: Dower, William J.
Barrett, Ronald W.
Cwirla, Steven E.
Duffin, David J.
Gates, Christian
Haselden, Sherril S.
Mattheakis, Larry C.
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                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Glaxo Wellcome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Dower, William J.
Barrett, Ronald W.
Cwirla, Steven E.
Duffin, David J.
Gates, Christian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: 919-248-1000 INFORMATION FOR SEQ ID NO: 17: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGIH: 15 amino acids
                                                                                                                                                                                                       Schatz, Peter J
                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 232
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 37.1
Best Local Similarity 100.
Matches 14; Conservative
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Patent No. 6083913
GENERAL INFORMATION:
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GENERAL INFORMATION:
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LENGIH:
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APPLICANT: Podduturi, Surekha
APPLICANT: Yin, Qun
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
TITLE OF INVENTION: RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37.1%; Score 73; DB 3; Length 15; 100.0%; Pred. No. 0.014; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/973,225A
FILING DATE: 04-Dec-1997
ATTORNEY FAGENT INFORMATION:
NAME: HINDIEC, RODERT T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3065USW
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 185:
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STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide
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SEQUENCE DESCRIPTION: SEQ ID NO: 185:
US-08-973-225-185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GEMERAL INFORMATION:
APPLICANT: Dower, William J.
APPLICANT: Barrett, Ronald W.
APPLICANT: Cwirla, Steven E.
APPLICANT: Gates, Christian
APPLICANT: Schatz, Peter J.
APPLICANT: Balasubramanian, Palaniappan
                                                                                        CITY: Research Triangle Park
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
NUMBER OF SEQUENCES: 232
                                                                                                                                                                               COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
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Best Local Similarity 100.
Matches 14; Conservative
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                        ZIP: 27709
                                                                                                           STATE: NC
                                                                                                                                     COUNTRY:
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APPLICANT:
APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37.1%; Score 73; DB 3; Length 15; 100.0%; Pred. No. 0.014; Live 0; Mismatches 0; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/244,298A
FILLIG DATE: 11-DEC-1996
CLASSIFICATION: 514
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APPLICANT: Barrett, Ronald W.
APPLICANT: Cwirla, Steven E.
APPLICANT: Gates, Christian
APPLICANT: Schatz, Peter J.
APPLICANT: Balasubramanian, Palaniappan
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/244,298A
FILING DATE: 11-DEC-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: HIUDIEC, ROBERT T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3281
TELECHONE: 919-248-1000: TELECHONE: 919-248-1000: INFORMATION FOR SEQ ID NO: 17:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Wagstrom, Christopher R. APPLICANT: Hendren, Richard W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 185, Application US/09244298A
; Patent No. 6121238
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Deprince, Randolph B. APPLICANT: Podduturi, Surekha APPLICANT: Yin, Qun
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STREET: Five Moore Drive, P.(
CITY: Research Triangle Park
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NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3
TELECOMMUNICATION: INFORMATION:
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INFORMATION FOR SEQ ID NO: 185:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                           15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.0
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-244-298A-17
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                                                                                                                                                                                                                                                                                                                 TYPE: amino acid STRANDEDNESS:
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15 amino acids

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RESULT 19
US-09-516-704-185
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Podduturi, Surekha
TITLE OF INVENTION: PRETIDES AND COMPOUNDS THAT BIND TO A
RECEPTOR
                                                                                                                                                  Length 15;
                                                                                                                                             37.1%; Score 73; DB 3; Length 15; 100.0%; Pred. No. 0.014; ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37.1%; Score 73; DB 4; Length 15; 100.0%; Pred. No. 0.014; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/516,704
FILING DATE: 01-Mar-2000
CLASSIFICATION: <UNknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P.O. Box 13398
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Balasubramanian, Palaniappan
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REGISTRATION NUMBER: 96,392
REFERENCE, DOCKET NUMBER: PK3281
TELECOMMUNICATION INFORMATION:
TELEPROME: 919-248-1000
INFORMATION FOR SEQ. ID NO: 17:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ) MOLECULE TYPE: peptide
) SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-516-704-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wagstrom, Christopher R.
Hendren, Richard W.
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STREET: Five Moore Drive,
                                                                                                                                                                                                                                                                                                                                                                      Sequence 17, Application US/09516704 Patent No. 6251864 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Dower, William J.
Barrett, Ronald W.
Cwirla, Steven E.
Gates, Christian
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STRANDEDNESS: <Unknown>
TOPOLOGY: linear
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                                                                                                                                                                                      14; Conservative
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Best Local Similarity 100.
Matches 14; Conservative
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-244-298A-185
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                                                                                                                                             Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
                                                                  APPLICANT: Dower, William J.
Barrett, Ronald W.
Cwirla, Steven E.
Gates, Christian
Schatz, Peter J.
Balasubramanian, Palaniappan
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APPLICATION NUMBER: US/09/516,704
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SEQUENCE DESCRIPTION: SEQ ID NO: 185:
US-09-516-704-185
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 185:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Research Triangle Park
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Sequence 185, Application US/09516704
Patent No. 6251864
GENERAL INFORMATION:
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; Patent No. 5869451
• Patent No. 5869451 5837683
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 15 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 37.1
Best Local Similarity 100.
Matches 14; Conservative
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APPLICANT: Dower,
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ADDRESSEE:
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                                                                                                       APPLICANT: Yin, Qun
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
TITLE OF INVENTION: RECEPTOR
NUMBER OF SEQUENCES: 244
CORRESPONDENCE ADDRESS:
ADDRESSEE: Glass Wellcome
ADDRESSEE: Glass Wellcome
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TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37.1%; Score 73; DB 2; Length 16; 100.0%; Pred. No. 0.014; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                            ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
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Barrett, Ronald W.

CWITLA, Steven E.

Gates, Christian
Schatz, Peter J.

Balasubramarian, Palaniappan
Wagstrom, Christopher R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COCATION: 15 COCATION: 15 OTHER INFORMATION: /product= "Beta-ala" US-08-764-640-18
                Balasubramanian, Palantappan
Wagstrom, Christopher R.
Hendren, Richard W.
Deprince, Randolph B.
Podduturi, Surekha
                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/764,640
FILING DATE: 11-DEC-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: HIUDIGE, RODGERT T.
REGISTRATION NUMBER: 36,392
                                                                                                                                                                                                                                                                                       COUNTRY: USA
2IP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 5869451
Patent No. 5869451 5837683
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Podduturi, Surekha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: Modified-site LOCATION: 15
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Best Local Similarity 100.
Matches 14; Conservative
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APPLICANT: DOWER,
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                                                      APPLICANT:
APPLICANT:
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APPLICANT:
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APPLICANT:
APPLICANT:
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                                    APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                37.1%; Score 73; DB 2; Length 16; 100.0%; Pred. No. 0.014; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/764,640
FILING DATE: 11-DEC-1996
CLASSIFICATION: 514
                NUMBER OF SEQUENCES: 244
CORRESPONDENCE ADDRESS:
ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: Five Moore Drive, P.O. Box 13398
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APPLICANT: Balasubramanian, Palaniappan
APPLICANT: Wagstrom, Christopher R.
APPLICANT: Hendren, Richard W.
APPLICANT: Deprince, Randolph B.
APPLICANT: Podduturi, Surekha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 232, Application US/08764640
patent No. 5869451
patent No. 5869451 5837683
                                                                                                            Research Triangle Park
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Barrett, Ronald W.
Cwirla, Steven E.
Gates, Christian
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Hrubiec, Robert T. REGISTRATION NUMBER: 36,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RECEPTOR
TITLE OF INVENTION: RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Glaxo Wellcome
                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 11-DEC-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 16 amino acids TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
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Matches 14; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                                                                                                            USA
                                                                                                                                                         COUNTRY: US
ZIP: 27709
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TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                               OTHER INFORMATION: /product= "Beta-ala"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: Five Moore Drive, P.O. Box 13398 CITY: Research Triangle Park
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/973,225A FILING DATE: 04-Dec-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: PK3065USW TELECOMMUNICATION INFORMATION: TELEPHONE: 919-248-1000 INFORMATION FOR SEQ ID NO: 194:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE DESCRIPTION: SEQ ID NO: 194:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
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Cwirla, Steven E.
Duffin, David J.
Gates, Christian
Haselden, Sherril S.
Mattheakis, Larry C.
Schatz, Peter J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 194, Application US/08973225A Patent No. 6083913 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Glaxo Wellcome
                                                                                                           Modified-site
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NAME: Hrubiec, Robert T.
                    STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: <Unknown>
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  TYPE: amino acid
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Best Local Similarity 100.
Matches 14: Conservative
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ZIP: 27709
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Best Local Similarity
                                                                                                           NAME/KEY:
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                                                                                                                               LOCATION
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                                                                                     FEATURE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 73; DB 2; Length 10; Pred. No. 0.014; 0; Indels
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                 SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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ADDRESSES: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
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ATTORNEY/AGENT INFORMATION:
NAME: H'UDIGC, ROBERT T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3065USW
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 37.1%; Score 73; DB Best Local Similarity 100.0%; Pred. No. 0.0 Matches 14; Conservative 0; Mismatches
                                                   PELICATION NUMBER: US/08/764,640
FILING DATE: 11-DEC-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INPORMATION:
NAME: HTMD16C, ROBERT T.
REGISTRATION NUMBER: 36,392
REFERRICE/DOCKET NUMBER: PK3281
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-11000
INPORMATION FOR SEQ. ID NO: 232:
SEQUENCE CHARACTERISTICS:
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Mattheakis, Larry C.
Schatz, Peter J.
PC-DOS/MS-DOS
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Barrett, Ronald W.
Cwirla, Steven E.
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INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                   16 amino acids
                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-764-640-232
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ZIP: 27709
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                     TYPE: amino acid STRANDEDNESS:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37.1%; Score 73; DB 3; Length 16; 100.0%; Pred. No. 0.014; tive 0; Mismatches 0; Indels
0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/973, 225A
FILING DATE: 04-Dec-1997
ATTORNEY AGENT INFORMATION:
NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36, 392
REFERENCE/DOCKET NUMBER: PK3065USW
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
SEQUENCE CHARACTERISTICS:
0; Mismatches
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MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 220:
US-08-973-225-220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Research Triangle Park
                                                                                                                                                                                                                            APPLICANT: Dower, William J.
Barrett, Ronald W.
Cwirla, Steven E.
Duffin, David J.
Gates, Christian
Haselden, Sherril S.
Mattheakis, Larry C.
                                                                                                                                                                    Sequence 220, Application US/08973225A Patent No. 6083913 GENERAL INFORMATION:
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STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 16 amino acids
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Best Local Similarity 100.
Matches 14; Conservative
Matches 14; Conservative
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                                                          2 IEGPTLROWLAARA 15
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                                      1 IEGPTLRQWLAARA 14
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US-09-244-298A-18
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                                                                                                                                    RESULT 25
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TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
TITLE OF INVENTION: RECEPTOR
NUMBER OF SEQUENCES: 244
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                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Glarow Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
APPLICANT: Cwirla, Steven E.
APPLICANT: Gates, Christian
APPLICANT: Schatz, Peter J.
APPLICANT: Balasubramanian, Palaniappan
APPLICANT: Wagstrom, Christopher R.
APPLICANT: Hendren, Richard W.
APPLICANT: Peddututi, Surekha
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Barrett, Ronald W.
Cwirla, Steven E.
Schatz, Christian
Schatz, Peter J.
Balasubramanian, Palaniappan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/244,298A FILING DATE: 11-DEC-1996 CLASSIFICATION: 514
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Hendren, Richard W.
Deprince, Randolph B.
Podduturi, Surekha
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                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 18:-
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: HTUDIEC, ROBERT T.
REGISTRATION NUMBER: 36,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid STRANDEDNESS:
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APPLICANT:
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APPLICANT:
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STATE:
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TELEPHONE: 919-248-1000 INFORMATION FOR SEQ ID NO: 18:
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ZIP: 27709
                                                                                                                                                                                                                                                                                                        TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                      linear
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TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A TITLE OF INVENTION: RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A TITLE OF INVENTION: RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37.1%; Score 73; DB 3; Length 16; 100.0%; Pred. No. 0.014; ative 0; Mismatches 0; Indels
                                                                                                                                                                                                        COMPUTER KEALBABLE FURK:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPOTER: IBM PC Compatible
CORPATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/244,298A
FILING DATE: 11-DEC-1996
CLASSIFTATE: TI-DEC-1996
CLASSIFTATE: NFORMATION:
MAME: HTUDIGC, ROBERT PK3281
FELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                  STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
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Balasubramanian, Palaniappan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 232, Application US/09244298A Patent No. 6121238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wagstrom, Christopher R.
Hendren, Richard W.
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Podduturi, Surekha
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IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Dower, William J. APPLICANT: Barrett, Ronald W. APPLICANT: Cwirla, Steven E. APPLICANT: Gates, Christian
                                     NUMBER OF SEQUENCES: 244
CORRESPONDENCE ADDRESS:
ADDRESSEE: Glaxo Wellcome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glaxo Wellcome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 16 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 14; Conserv
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                                                                                                                                                                           27709
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ZIP: 27709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-244-298A-194
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APPLICANT:
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APPLICANT:
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APPLICANT:
                                                                                                                                                                COUNTRY:
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                                                                                                                                         STATE:
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Podduturi, Surekha
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37.1%; Score 73; DB 3; Length 16; 100.0%; Pred. No. 0.014; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.30
PatentIn Release #1.0, Version #1.30
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Balasubramanian, Palaniappan
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APPLICATION NUMBER: US/09/516,704
FILING DATE: 01-Mar-2000
CLASSIFICATION: CURROWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: PK3281 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wagstrom, Christopher R.
Hendren, Richard W.
                                           APPLICATION NUMBER: US/09/244,298A FILING DATE: 11-DEC-1996 CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: Five Moore Drive, P. CITY: Research Triangle Park
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION: NAME: Hrubiec, Robert T.
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Barrett, Ronald W.
Cwirla, Steven E.
Gates, Christian
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                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: PKTELECOMMUNICATION INFORMATION:
TELEDHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 232:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 244
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                    CURRENT APPLICATION DATA:
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Best Local Similarity 100.
Matches 14; Conservative
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Gaps

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0; Indels

37.1%; Score 73; DB 4; Length 16; 100.0%; Pred. No. 0.014;

0; Mismatches

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Best Local Similarity 100.
Matches 14; Conservative
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US-08-764-640-195
                                                                                                                                                                                               US-09-516-704-232
Query Match
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Hendren, Richard W.
Deprince, Randolph B.
Podduturi, Surekha
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
                                                                                                                                                                                                                                                     37.1%; Score 73; DB 4; Length 16; 100.0%; Pred. No. 0.014; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/516,704
FILING DATE: 01-Mar-2000
CLASSIFICATION: <UNKNOWN>
                                                                                                                                             ; SEQUENCE DESCRIPTION: /product= "Beta-ala"; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: Five Moore Drive, P.O. Box 13398
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APPLICANT: Barrett, Ronald W.
CWilla, Steven E.
Gates, Christian
Schatz, Peter J.
Balasubramanian, Palaniappan
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MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 194:
US-09-516-704-194
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NAME: Hrubiec, Robert T.
RGASTERRATION NUMBER: 36,332
REFERENCE/DOCKET NUMBER: PK3281
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STATE: NC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 244
CORRESPONDENCE ADDRESS:
ADDRESSEE: Glaxo Wellcome
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TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 194:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 194, Application US/09516704 Patent No. 6251864 GENERAL INFORMATION:
                                                                                                            Modified-site
15
              TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: <Unknown>
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LENGTH: 16 amino acids
LENGTH: 16 amino acids
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                    NAME/KEY:
                                                                                                                                       LOCATION:
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                                                                                                   FEATURE
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Podduturi, Surekha
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37.1%; Score 73; DB 4; Length 16; 100.0%; Pred. No. 0.014; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                APPLICANT: Dower, William J.
Barrett, Ronald W.
Cwirla, Steven E.
Gatcs, Christian
Schatz, Peter J.
Balasubramanlan, Palaniappan
Wagstrom, Christopher R.
Hendren, Richard W.
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APPLICATION NUMBER: US/09/516,704
FILING DATE: 01-Mar-2000
FLASSIFICATION: <UNKnown>
ATTORNEY/AGENT INFORMATION:
NAME: Hrubiec, Robert T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 232:
US-09-516-704-232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: PK3281
TELECOMMUNICATION INPORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 232:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                          STREET: Five Moore Drive, P.C CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 36,392
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                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Glaxo Wellcome
Sequence 232, Application US/09516704 Patent No. 6251864 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                  RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 16 amino acids
                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 244
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                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
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Best Local Similarity 100.
Matches 14; Conservative
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TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A THROMBOPOIETIN RECEPTOR
APPLICANT: Yin, Qun
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
TITLE OF INVENTION: RECEPTOR
NUMBER OF SEQUENCES: 244
CORRESPONDENCE ADDRESS:
ADDRESSEE: Glaxo Wellcome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35.0%; Score 69; DB 2; Length 14; 100.0%; Pred. No. 0.036;
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                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/764,640
FILING DATE: 11-DEC-1996
CLASSIFICATION: 514
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                                                                                                                      STREET: Five Moore Drive, P.O. Box 13398 CITY: Research Triangle Park
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                                                                                                                                                                                                                                                                                                        11-DEC-1996
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Barrett, Ronald W.
Cwirla, Steven E.
Duffin, David J.
Gates, Christian
Haselden, Sherril S.
Mattheakis, Larry C.
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COMPUTER: IBM PC compatible
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                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Glaxo Wellcome
                                                                                                                                                                                                                                                                                                                                                                                                                                                         PK3281
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NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Schatz, Peter J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: PK
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 199:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 232
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COMPUTER READABLE FORM:
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LENGTH: 14 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 100.
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; MOLECULE TYPE: peptide US-08-764-640-199
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                                                                                                                                                                                     USA
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                                                                                                                                                           STATE: NC
COUNTRY: US
ZIP: 27709
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TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
TITLE OF INVENTION: RECEPTOR
NUMBER OF SEQUENCES: 244
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35.0%; Score 69; DB 2; Length 14; 100.0%; Pred. No. 0.036; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/764,640 FILING DATE: 11-DEC-1996 CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                  STREET: Five Moore Drive, P.O. Box 13398 CITY: Research Triangle Park
                                      Dower, William J.
Barrett, Ronald W.
Cwirla, Steven E.
Gates, Christian
Schatz, Peter J.
Balasubramanian, Palaniappan
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Balasubramanian, Palaniappan
Wagstrom, Christopher R.
Hendren, Richard W.
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Hendren, Richard W.
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Patent No. 5869451
Patent No. 5869451 5837683
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Podduturi, Surekha
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Podduturi, Surekha
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NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
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TELECOMNUNICATION:
TELEPHONE: 919-246-1000
INFORMATION FOR SEQ ID NO: 195:
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APPLICANT: Barrett, Ronald W.
APPLICANT: Cwirla, Steven E.
APPLICANT: Gates, Christian
                                                                                                                                                                                                                                                                                                                                    Glaxo Wellcome
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LENGTH: 14 amino acids
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Best Local Similarity 100.
Matches 13; Conservative
      Patent No. 5869451 5837683
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                        GENERAL INFORMATION:
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APPLICANT:
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APPLICANT:
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APPLICANT:
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MOLECULE TYPE: peptide US-09-244-298A-195
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CORRESPONDENCE ADDRESS:
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Best Local Similarity
Matches 13; Conserva
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           CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/973,225A
FILING DATE: 04-Dec-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: 96,392
TELECOMNUNICATION INFORMATION:
TELECOMNUNICATION INFORMATION:
TELECOMNUNICATION INFORMATION:
INFORMATION FOR SEQ ID NO: 195:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 35.0%; Score 69; DB 3; Length 14; Best Local Similarity 100.0%; Pred. No. 0.036; Matches 13; Conservative 0; Mismatches 0; Indels
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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ADDRESSES: Glazo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
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FILING DATE: 04-Dec-1997
ATTORNEY/AGENT INFORMATION:
NAME: HTUDIEC, ROBERT T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3065USW
TELECOMMUNICATION INRORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 199:
SEQUENCE CHARCTERISTICS:
                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 195:
US-08-973-225-195
OPERATING SYSTEM: PC-DOS/MS-DOS
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Mattheakis, Larry C.
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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Barrett, Ronald W.
Cwirla, Steven E.
Duffin, David J.
Gates, Christian
                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
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Best Local Similarity 100.0%; Pred. No. 0.036;
Matches 13; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Scharz, Peter J.
APPLICANT: Balsaubramanian, Palaniappan
APPLICANT: Wagstrom, Christopher R.
APPLICANT: Hendren, Richard W.
APPLICANT: Podduturi, Surekha
APPLICANT: Podduturi, Surekha
APPLICANT: Yin, Qun
TITLE OF INVENTION: RECEPTOR
STRANDEDNESS: CUNKNOWN>
STRANDEDNESS: CUNKNOWN>
TOPOLOGY: linear
SEQUENCE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 199:
US-08-973-225-199
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CLASSIFICATION: 514

TOWNEY/AGENT TANCE

AMPERICATION: 514
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REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 195:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Dower, William J.
APPLICANY: Barrett, Ronald W.
APPLICANY: Cwirla, Steven E.
APPLICANT: Gates, Christian
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MEDIUM TYPE: Floppy disk
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LENGTH: 14 amino acids
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                          Balasubramanian, Palaniappan
Wagstrom, Christopher R.
Hendren, Etchard W.
Deprince, Randolph B.
Podduturi, Surekha
INVENTION: BEPETIDES AND COMPOUNDS THAT BIND TO A
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Podduturi, Surekha
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
RECEPTOR
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                       NUMBER OF SEQUENCES: 244
CORRESPONDENCE ADDRESS:
ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
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Balasubramanian, Palaniappan
                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
RPPLICATION NUMBER: US/09/516,704
FILLING DATE: 01-Mar-2000
CLASSFIFICATION: <a href="https://doi.org/10.10m/">doi.org/</a>
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MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 195:
US-09-516-704-195
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Hendren, Richard W.
                                                                                                                                                                                                                                                                Research Triangle Park
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TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 195:
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ADDRESSEE: Glaxo Wellcome
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Barrett, Ronald W.
Cwirla, Steven E.
Gates, Christian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: <Unknown>
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        Schatz, Peter J.
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COMPUTER READABLE FORM:
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                                                                                                                                  TITLE OF
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TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
TITLE OF INVENTION: RECEPTOR
NUMBER OF SEQUENCES: 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35.0%; Score 69; DB 3; Length 14; 100.0%; Pred. No. 0.036; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/244,298A FILING DATE: 11-DEC-1996 CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
                                                                                                                                                                                                                                                                               Schatz, Peter J.
Balasubramanian, Palaniappan
Wagstrom, Christopher R.
Hendren, Richard W.
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Patent No. 6251864
GENERAL INFORMATION:
APPLICANT: DOWN: William J.
Barrett, Ronald W.
Cwirla, Steven E.
Gates, Christian
                                                                                                                         Sequence 199, Application US/09244298A Patent No. 6121238
GENERAL INFORMATION: APPLICANT: Dower, William J. APPLICANT: Barrett, Ronald W. APPLICANT: Cwirla, Steven E. APPLICANT: Gates, Christian
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BDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                 Deprince, Randolph B.
Podduturi, Surekha
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NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 919-248-1000 INFORMATION FOR SEQ ID NO: 199:
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LENGTH: 14 amino acids
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1 EGPTLROWLAARA 13
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                                                                                                       US-09-244-298A-199
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APPLICANT:
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APPLICANT: Yin, Qun
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
TITLE OF INVENTION: RECEPTOR
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100.0%; Pred. No. 0.038;
ative 0; Mismatches C
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CITY: Research Triangle Park
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APPLICANT: Balasubramanian, Palaniappan
APPLICANT: Wagstrom, Christopher R.
APPLICANT: Hendren, Richard W.
APPLICANT: Deprince, Randolph B.
APPLICANT: Podduturi, Surekha
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CLASSIFICATION: 514
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Patent No. 5869451
Patent No. 5869451 5837683
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CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: HYDDIG-C, RODERT T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK328
TELECOMMUNICATION INFORMATION:
TELEMONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 196: SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
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Barrett, Ronald W.
Cwirla, Steven E.
Gates, Christian
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ATTORNEY/AGENT INPORMATION:
NAME: H'UDDIEC, ROBERT T.
REGISTRATION NUMBER: 36,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: PK TELECOMMUNICATION INFORMATION:
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INFORMATION FOR SEQ ID NO: 200:
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                                                                                                                                                                                                                                                                                                           NAME/KEY: Modified-site LOCATION: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 35.0
Best Local Similarity 100.
Matches 13; Conservative
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                             amino acid
                                                                                                                                                                                                                                                        linear
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APPLICANT:
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APPLICANT:
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                                                                                                                                                                                                             TYPE:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Glaxo Wellcome STREET: Five Moore Drive, P.O. Box 13398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 35.0%; Score 69; DB 4; Length 14; Best Local Similarity 100.0%; Pred. No. 0.036; Matches 13; Conservative 0; Mismatches 0; Indels
                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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                                                                                                                                                              CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/516,704
FILING DATE: 01-Mar-2000
CLASSIFICATION: «Unknown»
ATTORNEY/AGENT INFORMATION:
NAME: HTUBLEC, RODERT T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: 96,392
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ. 1D NO: 199:
SEQUENCE CHARACTERISTICS:
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Balasubramanian, Palaniappan
Wagstrom, Christopher R.
Hendren, Richard W.
Deprince, Randolph B.
                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 199:
US-09-516-704-199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 196, Application US/08764640 Patent No. 5869451 Patent No. 5869451 5837683 GENERAL INFORMATION:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 14 amino acids
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Cwirla, Steven E.
Gates, Christian
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                                                                COMPUTER READABLE FORM:
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                       USA
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                         COUNTRY: US
ZIP: 27709
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US-08-764-640-196
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                                                                                    35.0%; Score 69; DB 2; Length 15; 100.0%; Pred. No. 0.038; tive 0; Mismatches 0; Indels
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            ; OTHER INFORMATION: /product= "N-methyl-Ala" US-08-764-640-209
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Balasubramanian, Palaniappan
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; OTHER INFORMATION: /product= "Sar"
US-08-764-640-215
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Hendren, Richard W.
                                                                                                                                                                                                                                                                                                 Sequence 215, Application US/08764640; Patent No. 5869451; Patent No. 5869451
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Podduturi, Surekha
Yin, Qun
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Barrett, Ronald W.
Cwirla, Steven E.
Gates, Christian
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 215:
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NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,3
REFERENCE/DOCKET NUMBER:
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Best Local Similarity 100.v
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LENGTH: 15 amino acids
                                                                                  Ouery Match
Best Local Similarity 100.0
Matches 13; Conservative
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APPLICANT: Dower,
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LOCATION: 14
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APPLICANT:
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APPLICANT:
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TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
TITLE OF INVENTION: RECEPTOR
NUMBER OF SEQUENCES: 244
                                                                                                                                                                                                                                              35.0%; Score 69; DB 2; Length 15; 100.0%; Pred. No. 0.038; attive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFFWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/764,640 FILING DATE: 11-DEC.1996 CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P.O. Box 13398
                                                                                                                                                                     ; OTHER INFORMATION: /product= "Beta-ala" US-08-764-640-200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schatz, Peter J.
Balasubramanian, Palaniappan
Wagstrom, Christopher R.
Hendren, Richard W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
REFERRNCE/DOCKET NUMBER: PK3281
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 209:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 209, Application US/08764640 Patent No. 5869451 Patent No. 5869451 Patent No. 5869451 5837683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Deprince, Randolph B.
Podduturi, Surekha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEE: Glaxo Wellcome
: Five Moore Drive, P.(
Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Dower, William J. APPLICANT: Barrett, Ronald W. APPLICANT: Cwirla, Steven E. APPLICANT: Gates, Christian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 11-DEC-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: Modified-site
                                                                                                                                 NAME/KEY: Modified-site LOCATION: 14
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                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.(
Matches 13; Conservative
                    LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS:
    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: peptide
                                                                            TOPOLOGY: linear
MOLECULE TYPE: peptide
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APPLICANT:
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APPLICANT:
APPLICANT:
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APPLICANT:
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GENERAL INFORMATION:
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Wrighton, Nicholas C.
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
THROMBOPOLETIN RECEPPOR
                                                                                                                                                                                                                                                                                                                                                                                 35.0%; Score 69; DB 3; Length 15; 100.0%; Pred. No. 0.038; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
STATE: NC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: /product- "Beta-ala" SEQUED.CE DESCRIPTION: SEQ ID NO: 196:
                                                                                                   Sequence 196, Application US/08973225A Patent No. 6083913 GENERAL INFORMATION:
                                                                                                                                                                                                           Haselden, Sherril S.
Mattheakis, Larry C.
Schatz, Peter J.
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; Sequence 200, Application US/08973225A
; Patent No. 6083913
                                                                                                                                       APPLICANT: Dower, William J.
Barrett, Ronald W.
Cwirla, Steven E.
Duffin, David J.
Gates, Christian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: 14
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: peptide
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Matches 13; Conservative
                     1 IEGPTLRQWLAAR 13
       1 IEGPTLROWLAAR 13
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                                                                         RESULT 44
US-08-973-225-196
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Wagstrom, Christopher R.
Wrighton, Nicholas C.
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
THROMBOPOLETIN RECEPTOR
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35.0%; Score 69; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.038;
Matches 13; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPATIBL SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: /product= "Beta-ala" SEQUENCE DESCRIPTION: SEQ ID NO: 200:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/973,225A
FILING DATE: U4-Dec-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3065USW
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 200:
SEQUENCE CHARACTERISTICS:
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                                                                                                                 Haselden, Sherril S.
Mattheakis, Larry C.
APPLICANT: Dower, William J.
Barrett, Ronald W.
Cwirla, Steven E.
Duffin, David J.
Gates, Christian
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STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 15 amino acids
                                                                                                                                                                                                                                                                              SEQUENCES: 232
                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 27709
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                        STATE: NC
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 EGPTLRQWLAARA 13
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

; Search time 23.99 Seconds
(without alignments)
111.156 Million cell updates/sec December 26, 2001, 10:25:08 Run on:

US-09-422-838C-33 197 Title: Perfect score:

1 IEGPTLRQWLAARAGGCCGGGGIEGPTLRQWLAARA 36

Sednence:

522463 segs, 74073290 residues Searched:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 100 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	TPO-mimetic peptid	TPO-mimeric peptid				I .	I	Thrombopoietin mim	Thrombopoietin mim	TPO-mimetic peptid	Thrombopoietin mim
T WITH TOO	OI.	AAB17303	AAB1/30/	AAY96524	AAB17305	AAB16963	AAB17293	AAB17301	AAY96523	AAY96525	AAB17302	AAY96528
	DB	21	7.7	21	21	21	21	21	21	21	21	21
	% Query Match Length DB	36	36	36	39	36	36	36	36	36	40	41
	% Query Match	100.0	100.0									
	Score	197	197	197	185.5	185	185	185	185	185	185	185
	Result No.	7	7	m	4	S	9	7	80	6	10	11

PO-mimetic PO-mimetic FO-mimetic FO-mimetic TM NT-TMD-FC PM MP-TWD-FC PM MP-TWD-FC PM MP-TWD-FC PM MP-TWD-PC PC-MIMETIC PC-MIMETIC PC-MIMETIC PO-MIMETIC PO-MIMETIC	ic pep lic pep		c c pe ettin ettin ettin ettin ettin ettin ettin ettin ettin ettin ettin ettin
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221 221 221 221 221 221 221 221 221	222222222222222222222222222222222222222		22118 22118 2219 2219 2219 2219 2219 221
44440000 2000 00000 0000000000000000000	0 4 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	29 28 31 31 28 29 20 20 20 20 24 14 14 14 14	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4
	2.1.2.2.2.2.2.2.2.2.2.2.2.2.2.2		1.77 2.37 2.47 2.47 2.47 2.47 2.47 2.47 2.47 2.4
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112 113 114 114 119 119 122 123 144	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	0 1 1 2 4 4 4 4 4 4 4 4 5 5 5 5 5 5 5 5 5 5 5	\$\(\rightarrow\) \(\rightarrow\) \(\rightarrow

Peptide chain of c	Thrombopoietin rec	Thrombopoietin rec	Neurotrophic facto	Peptide chain of c	Human ORFX ORF1058	NT-4 amino acid se	Neurotrophic facto	Neurotrophic facto	Neurotrophic facto	Human neurotrophin	Human neutrophin-4	Human neurotrophin	Neurotrophic facto	Neurotrophic facto	Neurotrophic facto
AAW66717	AAW36781	AAW36782	AAR22471	AAW66731	AAB41294	AAB35947	AAR22469	AAR22479	AAR22481	AAW48890	AAB29112	AAY92009	AAR22472	AAR22465	AAR22482
19	18	18	13	19	21	22	13	13	13	19	21	21	13	13	13
15	12	14	130	15	146	118	130	130	130	130	130	130	142	210	210
33.0	32.5	32.5	31.2	31.0	31.0	30.7	30.7	30.7	30.7	30.7	30.7	30.7	30.7	30.7	30.7
65	64	64	61.5	61	61	60.5	60.5	60.5	60.5	60.5	60.5	60.5	60.5	60.5	60.5
85	98	87	88	83	06	16	95	93	94	92	96	97	98	66	100

## ALIGNMENTS

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The present invention describes composition of matter (I) comprising an (XI)a-F1-(X2)b, where FI = an FC domain; XI and X2 = are each independently selected from (LI)c-P1-(L2)d-P2, (LI)c-P1-(L2)d-P2, (LI)c-P1-(L2)d-P2, (LI)c-P1-(L2)d-P2, (LI)c-P1-(L2)d-P2, (LI)c-P1-(L2)d-P2, (LI)c-P1-(L2)d-P2, (LI)c-P1-(L2)d-P2-(LI)c-P1-(L2)d-P2-(LI)c-P1-(L2)d-P2-(LI)c-P1-(L2)d-P2-(LI)c-P1-(L2)d-P2-(LI)c-P1-(L2)d-P2-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c-P1-(LI)c
                                                                                                                                                                                                                                                         Modified peptide, therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoletin; thrombopoletin; interleukin 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                 cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                               TPO-mimetic peptide sequence SEQ ID NO:359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1; Page 322; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            asthma; thrombosis; pharmaceutical.
AAB17303 standard; Peptide; 36 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Feige U, Liu C, Cheetham J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99WO-US25044
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                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (AMGE-) AMGEN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200024782-A2.
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                                                                                                                              31-OCT-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic
                                                             AAB17303;
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             useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor blading, protein A binding, complement fixation, and possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes composition of matter (I) comprising an (X_1)a_{-1}(-X_2)b_{-1} where (I) is: (X_1)a_{-1}(-X_2)b_{-1} where (I) is: (X_1)a_{-1}(-X_2)b_{-1} where (I) = an FC domain, X_1 and X_2 = are each independently selected from -(L_1)c_{-1}p_{-1}(L_2)d_{-1}p_{2}. -(L_1)c_{-1}p_{-1}(L_2)d_{-1}p_{2}. -(L_1)c_{-1}p_{-1}(L_2)d_{-1}p_{2}. where P_1, P_2, P_3, and P_4 = are each independently sequences of pharmacologically active peptides; L_1, L_2, L_3, and L_4 = are each independently linkers; and a, b, c, d, e, and f = are each independently 0 or 1, provided that at least 1 of a and b is 1. The composition can have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are
be used for producing pharmaceutical compositions. The compositions are
                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; minetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                             Length 36;
                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                             Score 197; DB 21;
Pred. No. 1.5e-16;
                                                                                                                                                                                       100.0%; Scc...
100.0%; Pred. No. ...
0; Mismatches
                                                                                                                                                                                                                                                                                       36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TPO-mimetic peptide sequence SEQ ID NO:363.
                                                                                                                                                                                                                                                                                                           1 IEGPTLRQWLAARAGGGCGGGGIEGPTLRQWLAARA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 1; Page 324; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                        AAB17307 standard; Peptide; 36 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cheetham J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99WO-US25044.
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99US-0428082.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-OCT-2000 (first entry)
                                                                                                                                                                                                           Ouery Match 100.
Best Local Similarity 100.
Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    autoimmune diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-350702/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (AMGE-) AMGEN INC.
                                                                                                                                                   36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200024782-A2
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22-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB17307;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Feige U,
                                                                                                                                                                                                                                                                                                                                                                                  7
                                                                                                                                                                                                                                                                                                                                                                                                      AAB17307
                                                                                                                                                                                                                                                                                                                                                                                    RESULT
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useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69443 to AAA69526 and AAB18035 to AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thrombopoietin; mimetic; TMP; TPO; platelet; megakaryocyte; production; anti-human immunodeficiency virus; anti-HIV; anti-anemic; dermatological; immunosuppressive; anti-inflammatory; linker; cyclic; linear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Thrombopoietic peptides which activate mpl receptors and increase the production of platelets or platelet precursors, useful for treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A compound which binds to an mpl receptor comprising a thrombopoietin mimetic peptide (TMP) dimer joined by a linker [TMP_1-(L_1)_nTMP_2], is new. TMP_1 and TMP_2 are amino acid sequences varying from at least lot of 14 residues in length comprising X_2 - X_{1-1}, X_2 - X_{1-1}, X_2 - X_{1-1}, X_2 - X_{1-1}, X_1 - X_{1-1}, X_1 - X_{1-1}, X_1 - X_{1-1}, and X_1 - X_{1-1}, X_1 - X_1, X_1 - X_1, X_2 - X_1, and X_1 - X_1 - X_1, X_1 - X_1, X_2 - X_1, and X_1 - X_1 - X_1, X_2 - X_1, X_3 - X_1, and
                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                      0
                                                                                                                                                                        Length 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "optionally linked to an Fc molecule"
                                                                                                                                                                                                      Indels
                                                                                                                                                                     Query Match 100.0%; Score 197; DB 21; Best Local Similarity 100.0%; Pred. No. 1.5e-16; Matches 36; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                       1 IEGPTLRQWLAARAGGGCGGGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                         Thrombopoietin mimetic peptide compound 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         production of platelets or platelet prdiseases which involve thombocytopenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "optional"
15..22
/label= linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 16; Page 62; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                          AAY96524 standard; peptide; 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= TMP_1
9..31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23..36
/label= TMP_2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Feige U, Cheetham J;
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                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (AMGE-) AMGEN INC.
                                                                                                                   36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200024770-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-OCT-1999;
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                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                           AAY96524;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Liu C,
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   8.56666666
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o;
\chi_{-4} = P; \chi_{-5} = T or S; \chi_{-6} = L, I, V, A or F; \chi_{-7} = R or K; \chi_{-8} = Q, N, D, E, S, T, K, H, or E; \chi_{-11} = L, I, V, A, F, M, or K; \chi_{-11} = R, I, V, L, F, G, S, Or Q; \chi_{-13} = R, K, T, V, N, Q or G; \chi_{-14} = A, I, V, L, F, T, R, E, or G; L_{-1} = 1 inker of omprising 1 to 20 amino acids; and n = 0 or 1. The compounds bind to and activate the C-Mpl receptor which mediates the activity of endogenous thrombopoietin. The TMPs are useful for increasing the production of platelets or platelet precursors (e.g. megakaryocytes) in a mammal, which is useful for treatment of diseases which involve thombocytopenia, e.g. aplastic anaemia, immune thrombocytopenia (ITP), human immunodeficiency
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes composition of matter (I) comprising an FC domain, pharmacologically active peptides, and linkers. Where (I) is: (X1)a-F1-(X2)b, where: F1 = an FC domain; X1 and X2 = are each independently selected from -(L1)c-P1-(L2)d-P2, -(L3)e-P2, -(L1)c-P1-(L2)d-P2-(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3, and P4 = are each independently sequences of pharmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently
                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VBGF; immunosuppressive; EPO; TPO; CTLA4; minetic; IL-1; TRF: antagonist; MMF; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                            Length 36;
                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modified peptide; therapeutic agent; fusion; Fc domain;
                                                                                                                                                             is useful for treatment of diseases which involve thombaplastic anaemia, immune thrombocytopenia (ITP), human virus associated ITP, and systemic lupus erythematosus.
                                                                                                                                                                                                                                                                                                            100.0%; Score 197; DB 21; 100.0%; Pred. No. 1.5e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                 1 IEGPTLRQWLAARAGGGCGGGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TPO-mimetic peptide sequence SEQ ID NO:361.
                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1; Page 323; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                asthma; thrombosis; pharmaceutical.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB17305 standard; Peptide; 39
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                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 36; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                   36 AA;
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22-OCT-1999;
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                                                                                                                                                                                                                                                 Sequence
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us-09-422-838c-33.rag

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O or 1, provided that at least 1 of a and b is 1. The composition can have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69443 to AAA69526 and AAB18093 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes composition of matter (I) comprising an Fc domain, pharmacologically active peptides, and linkers. Where (I) is: (X1)a *Fl-(X2)b, where: F1 = an Fc domain, X1 and X2 = are each independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2, -(L1)d-P2, (L1)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P2-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 185..,
Pred. No. 3.7e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                        94.2%; Score 185.5; DB 21; 92.3%; Pred. No. 3.7e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 IEGPTLRQWLAARAGGGC----GGGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          asthma; thrombosis; pharmaceutical.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Feige U, Liu C, Cheetham J,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 autoimmune diseases -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                               39 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200024782-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69443 to AAA69526 and AAB180955 to AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; mmmp; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                         ;
                                                                                                                                                                                                                                                              Length 36;
                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                              Score 185; DB 21;
Pred. No. 3.9e-15;
                                                                                                                                                                                                                                                                                                                                                                   1 IEGPTLRQWLAARAGGGCGGGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TPO-mimetic peptide sequence SEQ ID NO:349.
                                                                                                                                                                                                                                                                                                     0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB17293 standard; Peptide; 36
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                                                                                                                                                                                                                                                                93.98;
97.28;
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99US-0428082.
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Best Local Similarity 97.29
Matches 35; Conservative
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be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
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(X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each
independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2,
-(L1)c-P1-(L2)d-P2-(L3)e-P^3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4
where P1, P2, P3, and P4 = are each independently sequences of
pharmacologically active peptides; L1, L2, L3, and L4 = are each
independently linkers; and a, b, c, d, e, and f = are each independently
or 1, provided that at least, of and b is 1. The composition can
have cytostatic, antiasthmatic, thrombolytic and immunosuppressive
activities. DNAs, vectors and host cells from the present invention can
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activities. DNAs, vectors and host cells from the present invention can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; asthma; thrombosis; pharmaceutical.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
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                                                                                                                                                                                                                                                                                                                                                                                                             ); DB 21;
3.9e-15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 IEGPTLRQWLAARAGGGCGGGGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                             Score 185;
Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Feige U, Liu C, Cheetham J, Boone TC;
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                                                                                                                                                                                                                                                                                                                                                                                                                 93.98;
97.28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 35; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (AMGE-) AMGEN INC
                                                                                                                                                                                                                                                                                                             36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200024782-A2.
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                                                                                                                                                                                                                                                                                                                    Sequence
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             useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69443 to AAA69526 and AAB18055 to AAAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thrombopoietin; mimetic; TMP; TPO; platelet; megakaryocyte; production; anti-human immunodeficiency virus; anti-HIV; anti-anemic; dermatological; immunosuppressive; anti-inflammatory; linker; cyclic; linear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Thrombopoietic peptides which activate mpl receptors and increase the production of platelets or platelet precursors, useful for treatment of diseases which involve thombocytopenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A compound which binds to an mpl receptor comprising a thrombopoietin mimetic peptide (TMP) dimer joined by a linker [TMP_1-(L_1)_nTMP_2], is new. TMP_1 and TMP_2 are amino acid sequences varying from at least 10 to 14 residues in length comprising x_2-x_1_0, x_2-x_1_1, x_2-x_1_2, x_2-x_1_3, x_2-x_1_4, x_1-x_1-x_1-0, x_1-x_1-1, x_1-x_1-2, x_1-x_1-3, and
be used for producing pharmaceutical compositions. The compositions are
                                                                                                                                                                                                      Gaps
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                                                                                                                                                                        Length 36;
                                                                                                                                                                                                      Indels
                                                                                                                                                                        DB 21;
                                                                                                                                                                     Score 185; DB 21;
Pred. No. 3.9e-15;
0; Mismatches 1
                                                                                                                                                                                                                                   1 IEGPTLRQWLAARAGGGGGGGGGGEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                    Thrombopoietin mimetic peptide compound 4.
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                                                                                                                                                                                                                                                                                                                                              AAY96523 standard; peptide; 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15..22
/label= linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'label= TMP_1
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/label= TMP_2
                                                                                                                                                                     93.98;
97.28;
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                                                                                                                                                                     Query Match 93.9
Best Local Similarity 97.2
Matches 35; Conservative
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                                                                                                                       36 AA;
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X_1-X_1_4. X_1 = I, A, V, L, S or R; X_2 = E, D, K or V; X_3 = G or A; or E; X_4 = P; X_5 = T or S; X_6 = L, I, V, A or F; X_7 = R or K; X_8 = Q, N, or E; X_9 = W, Y or F; X_1_0 = L, I, V, L, F, M, or K; X_1_1 = A, I, V, L, F, G, S, or Q; X_1_3 = R, K, L, V, N, Q or G; X_1_4 = A, I, V, L, F, T, R, E, or G; L_1 = linker comprising 1 to 20 amino acids; and n = 0 or 1. The compounds bind to and activate the c-Mpi receptor which mediates the activity of endogenous thrombopotetin. The TMPs are useful for increasing the production of platelete or platelet precursors (e.g. megakaryocytes) in a mammal, which is useful for treatment of diseases which involve thombocytopenia, e.g. aplastic anaemia, immunoelytopenia (ITP), human immunodeficiency
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thrombopoietin; mimetic; TMP; TPO; platelet; megakaryocyte; production; anti-human immunodeficiency virus; anti-HIV; anti-anemic; dermatological; immunosuppressive; anti-inflammatory; linker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Thrombopoietic peptides which activate mpl receptors and increase the production of platelets or platelet precursors, useful for treatment of diseases which involve thombocytopenia
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                                                                                                                                                                                                                                               Length 36;
                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                       virus associated ITP, and systemic lupus erythematosus.
                                                                                                                                                                                                                                               DB 21;
                                                                                                                                                                                                                                              93.9%; Score 185; DB 21; 97.2%; Pred. No. 3.9e-15;
                                                                                                                                                                                                                                                                                                       1 IEGPTLRQWLAARAGGGCGGGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Thrombopoietin mimetic peptide compound 6.
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/label= linker
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/label- TMP_2
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                                                                                                                                                                                                                                                                           35; Conservative
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Best Local Similarity
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                                                                                                                                                                                                     36 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200024770-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                      Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                      93.9%; Score 185; DB 21; Length 36; ilarity 97.2%; Pred. No. 3.9e-15; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                1 IEGPTLRQWLAARAGGGCGGGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                           TPO-mimetic peptide sequence SEQ ID NO:358.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      asthma; thrombosis; pharmaceutical.
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                                                                                                                                                                                                                                                                                                                                       AAB17302 standard; Peptide;
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99US-0428082
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         autoimmune diseases
                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 35; Conserv
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Claim 16; Page 65; 91pp; English.

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independently selected from -(L1)c-P1. (L2)d-P2. (L2)d-P2. (L2)d-P2. (L2)d-P2. (L3)d-P2. (L3)d-P3. (L4)f-P4 where P1, P2, P3, and P4 = are each independently sequences of planmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently of or 1, provided that at least 1 of a and b is 1. The composition can have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can be useful for treating pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Pc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Pc receptor binding, protein (and possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to AAB1803 represent invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thrombopoietin; mimetic; TMP; TPO; platelet; megakaryocyte; production; anti-human immunodeficiency virus; anti-HIV; anti-anemic; dermatological; immunosuppressive; anti-inflammatory; linker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Thrombopoietic peptides which activate mpl receptors and increase the production of platelets or platelet precursors, useful for treatment of diseases which involve thombocytopenia
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                                                                                                                                                                                                                                                                                                                                                                                           Length 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                       Score 185; DB 21;
Pred. No. 4.3e-15;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 IEGPTLRQWLAARAGGG----CGGGGIEGPTLRQWLAARA 36
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/label= linker
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/label= TMP_2
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                                                                                                                                                                                                                                                                                                                                                                                           93.9%;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                       Sequence
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platelets or platelet precursors (e.g. megakaryocytes) in a mammal, which is useful for treatment of diseases which involve thombocytopenia, e.g. aplastic anaemia, immune thrombocytopenia (ITP), human immunodeficiency
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93.9%; Score 185; DB 21; 97.2%; Pred. No. 4.4e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 iegptlrqwlaaragggggggggegptlrqwlaara 41
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                                                                                                                                                                                                                                            useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
The present invention describes composition of matter (I) comprising an FC domain, pharmacologically active peptides, and linkers. Where (I) is: (X1)a-F1-(X2)b, where: F1 = an FC domain, X1 and X2 = are each independently selected from -(Li)c-P1-(L2)d-P2, (L3)a-P2-(L3)a-P2, (L1)c-P1-(L2)d-P2-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)a-P3-(L3)and L4 = are each independently sequences of pharmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and ab, c. d, e, and f = are each independently linkers; and ab, c. d, e, and f = are composition can have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        present invention describes composition of matter (I) comprising an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
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Pred. No. 4.5e-15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer labil-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AA69443 to AAA69526 and AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
Fc domain, pharmacologically active peptides, and linkers. Where (I) is:

(X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each
independently selected from -(L1)c-P1-(L2)d-P2.

-(L1)c-P1-(L2)d-P2-(L3)d-P2, or -(L1)c-P1-(L2)d-P2-(L3)e-P3.

where P1, P2, P3, and P4 = are each independently sequences of pharmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently or 1, provided that at least 1 of a and b is 1. The composition can have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are more in the present invention and confine in the present invention can be used for producing pharmaceutical compositions. The compositions are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93.9%; Score 185; DB 21; Length 42; 97.2%; Pred. No. 4.5e-15;
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0; Mismatches
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99US-0428082
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Best Local Similarity
Matches 35; Conserv
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The present invention describes composition of matter (I) comprising an

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CC (X1)a-F1 (X2)b, where: F1 = an Fc domain; X1 and X2 = are each independently selected from -[(1)c-P1, -[(1)c-P1-(12)d-P2].

CC (X1)a-F1 (Z2)b, where: F1 = an Fc domain; X1 and X2 = are each independently selected from -[(1)c-P1, -[(1)c-P1-(12)d-P2].

CC -(L1)c-P1 (L2)d-P2-(L3) =-P3-(L4)f-P4

CC where P1, P2, P3, and P4 = are each independently sequences of pharmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and ast 1 of a and b is 1. The composition can consist in the present invention and because of a receptor binding, protein a per use of an Fc domain (rather than a Fab domain) can provide a longer consisting cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer consisting complement fixation, and possibly placental transfer. AAA69443 conduction, and possibly placental transfer. AAA69443 conductors used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Immunoglobulin; IgG1; Fc; thrombopoietin; mimetic; TMP; TPO; platelet; megakaryocyte; production; anti-human immunodeficiency virus; anti-HIV; anti-anaemic; dermatological; immunosuppressive; anti-inflammatory.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              production of platelets or platelet precursors, useful for treatment of diseases which involve thombocytopenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Overlapping oligonucleotides were used to construct a synthetic gene encoding a thrombopoietin mimetic peptide (TMP), which was then fused in-frame to the Fc region of the human igdl chain (see AAY96529). A compound which binds to an mpl receptor comprising a TMP dimer joined by a linker [PIMP_1 (L_1)_mTMP_2], is new. TMP_1 and TMP_2 are amino acid sequences varying from at least 10 to 14 residues in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thrombopoietic peptides which activate mpl receptors and increase the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 185; DB 21; Length 42; Pred. No. 4.5e-15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 IEGPTLRQWLAARAGGGCGGGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93.98;
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Best Local Similarity
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length comprising X_2-X_1_0, X_2-X_1_1, X_2-X_1_2, X_2-X_1_3, X_2-X_1_4, X_1-X_1_0, X_1-X_1_1, X_1-X_1_3, and X_1-X_1_4, X_1-1, A, X_1-1, A, X_1-1, X_2-1, X_2-1, X_2-1, X_3-1, X
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic: VEGF; immunosuppressive; BPO; TPO; CTLA4; minetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic IMP-TMP-Fc gene construction peptide SEQ ID NO:385.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 185; DB 21;
Pred. No. 4.5e-15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 IEGPTLRQWLAARAGGGCGGGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB17311 standard; Peptide; 60 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93.98;
97.28;
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99US-0428082
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 97.24
Matches 35; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                       42 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200024782-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB17311;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB17311
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-(LL)c-Pl-(L2)d-P2-(L3)e-P-3, or -(L1)c-Pl-(L2)d-P2-(L3)e-P3-(L4)f-P4

where Pl, P2, P3, and P4 = are each independently sequences of
pharmacologically active peptides; L1, L2, L3, and L4 = are each
independently linkers; and a, b, c, d, e, and f = are each independently

or 1, provided that at least i of a and b is 1. The composition can
have eytostatic, antiasthmatic, thrombolytic and immunosuppressive
activities. DNAs, vectors and host cells from the present invention can
be used for producing pharmaceutical compositions. The compositions are
useful for treating cancer, asthma, thrombosis, or autoimmune diseases.
The use of an Fc domain (cather than a Fab domain) can provide a longer
half-life or incorporate functions such as Fc receptor binding, protein
A binding, complement fixation, and possibly placental transfer. AAA69443

c to AAA69526 and AAB18003 represent nucleotide and amino acid
sequences used in the exemplification of the present invention.
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\$

60 AA; Sequence

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0
                                      0;
      Length 60;
                                  1; Indels
 93.9%; Score 185; DB 21;
97.2%; Pred. No. 6.4e-15;
1ve 0; Mismatches 1;
                                                           1 IEGPTLRQWLAARAGGGCGGGGIEGPTLRQWLAARA 36
                                                                                 2 iegptlrqwlaaragggggggggiegptlrqwlaara 37
Ouery Match
Best Local Similarity 97.28
Matches 35; Conservative
                                                               õ
                                                                                           Db
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AAB16960 standard; Protein; 269 AA. 31-OCT-2000 (first entry) AAB16960; AAB16960 

Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMF; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; TMP-TMP-Fc protein sequence SEQ ID NO:10. asthma; thrombosis; pharmaceutical.

Homo sapiens. Synthetic. WO200024782-A2.

04-MAY-2000

99WO-US25044. 25-OCT-1999;

98US-0105371. 99US-0428082. 23-OCT-1998; 22-OCT-1999;

(AMGE-) AMGEN INC.

Feige U, Liu C, Cheetham J, Boone TC;

Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and WPI; 2000-350702/30. N-PSDB; AAA69446.

Example 2; Page 185-186; 608pp; English.

autoimmune diseases

The present invention describes composition of matter (I) comprising an Fc domain, pharmacologically active peptides, and linkers. Where (I) is: (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each

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independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2,
-(L1)c-P1-(L2)d-P2-(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4
-(L1)c-P1-(L2)d-P2-(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4
-(L1)c-P1-(L2)d-P2-(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4
-(L1)c-P1-(L2)d-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4
-(L1)c-P1-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-(L3)d-P3-
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                                                           Gaps
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Query Match 93.9%; Score 185; DB 21; Length 269; Best Local Similarity 97.2%; Pred. No. 2.9e-14; Matches 35; Conservative 0; Mismatches 1; Indels 0
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1 IEGPTLRQWLAARAGGGCGGGGIEGPTLRQWLAARA 36 2 iegptlrqwlaaraggggggggegptlrqwlaara 37 δŽ Db

RESULT 18

AAY96531 standard; Protein; 269 AA. AAY96531

AAY96531;

04-SEP-2000 (first entry)

Human IgG1 Fc TMP fusion protein.

Immunoglobulin; IgG1; Fc; thrombopoietin; mimetic; TMP; TPO; platelet; megakaryocyte; production; anti-human immunodeficiency virus; anti-HIV; anti-anaemic; dermatological; immunosuppressive; anti-inflammatory.

Homo sapiens.

WO200024770-A2.

04-MAY-2000.

99WO-US24834. 22-OCT-1999;

23-OCT-1998;

(AMGE-) AMGEN INC.

Liu C, Feige U, Cheetham J;

WPI; 2000-365108/31. N-PSDB; AAA29229.

Thrombopoietic peptides which activate mpl receptors and increase the production of platelets or platelet precursors, useful for treatment of diseases which involve thombocytopenia 

Example 2A; Page 49-50; 91pp; English.

A compound which binds to an mpl receptor comprising a thrombopoietin mimetic peptide (TMP) dimer joined by a linker [TMP.1-(L.1).nTMP.2], is new. TMP.1 and TMP.2 are amino acid sequences varying from at least 10 to 14 residues in length comprising  $X_2 - X_1 = 0$ ,  $X_2 - X_1 = 1$ ,  $X_2 - X_2 = 1$ ,  $X_2 - X_2 = 1$ ,  $X_2 - X_3 = 1$ ,  $X_3 - X_3$ 

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L, F, S, T, K, H, or E; x_{-1} = A, I, V, L, F, G, S, or Q; x_{-1} = B, K, comprising 1 to 20 amino acids; and n = 0 or 1. The compounds bind to and activate the C-Mpl receptor which mediates the activity of endogenous thrombopoietin. The TMPs are useful for increasing the production of platelets or platelet precursors (e.g. megakaryocytes) in a mammal, which is useful for treatment of diseases which involve thombocytopenia, e.g. aplastic anaemia, immune thrombocytopenia (ITP), human immunodeficiency virus associated ITP, and systemic lupus erythematosus.
                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes composition of matter (I) comprising an KC domain, pharmacologically active peptides, and linkers. Where (I) is: (X1)a-F1-(X2)b, where F1 = an Fc domain, X1 and X2 = are each independently selected from -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, -(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 pharmacologically active peptides: L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently
                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                          Length 269;
                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                       Score 185; DB 21;
Pred. No. 2.9e-14;
                                                                                                                                                                                                                                                                                                                                 234 iegptlrqwlaaragggggggggegptlrqwlaara 269
                                                                                                                                                                                                                                                                                                              1 IEGPTLRQWLAARAGGGCGGGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                          0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fc-TMP-TMP protein sequence SEQ ID NO:8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB16959 standard; Protein; 268 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Feige U, Liu C, Cheetham J,
                                                                                                                                                                                                                                     93.98;
97.28;
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                                                                                                                                                                                                                                                         Local Similarity 97.2 nes 35; Conservative
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                                                                                                                                                                                      269 AA;
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                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB16959;
                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 19
                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                           AAB16959
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O or 1, provided that at least 1 of a and b is 1. The composition can have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69443 to AAA69526 and AAB18093 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes composition of matter (I) comprising an FC domain, pharmacologically active peptides, and linkers. Where (I) is: (X1)a-F1-(X2)b, where: FI = an FC domain; X1 and X2 = are each independently selected from -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, -(L3)e-P^3, and P4 = are each independently sequences of pharmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently or 1, provided that at least 1 of a and b is 1. The composition can
                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; minetic; IL-1; TNR: antagonist; mmyp; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  peptide; therapeutic agent; fusion; Fc domain; cancer;
                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                           Length 268;
                                                                                                                                                                                                                                                                     Score 181; DB 21; Length 2 Pred. No. 8.4e-14; 0: Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                         234 iegptlrqwlaaraggggggggggegptlrqwlaar 268
                                                                                                                                                                                                                                                                                                                                                       1 IEGPTLRQWLAARAGGGGGGGGGIEGPTLRQWLAAR 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TPO-mimetic peptide sequence SEQ ID NO:362.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; Page 324; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     asthma; thrombosis; pharmaceutical.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB17306 standard; Peptide; 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cheetham J,
                                                                                                                                                                                                                                                                           91.98;
97.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99WO-US25044
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                                                                                                                                                                                                                                                                                                               34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-350702/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  autoimmune diseases
                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (AMGE-) AMGEN INC.
                                                                                                                                                                                                                  268 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200024782-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                                                                                                      Seguence
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                                                                                                                                                                                                                                                                                                                   Matches
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useful for treating cancer, astima, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer than 11-11fe or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69443 to AAA69526 and AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are
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36 AA; Sequence

Gaps ; 0 DB 21; Length 36; Indels 2e-14; 1 IEGPTLRQWLAARAGGGCGGGGIEGPTLRQWLAARA 36 Pred. No. 2e-1 0; Mismatches 90.9%; Score 179; 94.4%; Pred. No. 20 Best Local Similarity 94.4 Matches 34; Conservative Query Match ò

AAY96526 standard; peptide; 36 AAY96526;

Z

(first entry) 04-SEP-2000 Thrombopoietin mimetic peptide compound 7.

Thrombopoietin; mimetic; TMP; TPO; platelet; megakaryocyte; production; anti-human immunodeficiency virus; anti-HIV; anti-anemic; dermatological; immunosuppressive; anti-inflammatory; linker.

Synthetic

'note= "optionally linked to an Fc molecule" Location/Qualifiers 15..18 /label= linker 'label= TMP\_1 Modified-site Peptide Peptide 

WO200024770-A2

19..32 /label= TMP\_2

Peptide

04-MAY-2000

99WO-US24834 22-OCT-1999;

98US-0105348 23-OCT-1998;

(AMGE-) AMGEN INC.

Feige U, Cheetham J; Liu C,

WPI; 2000-365108/31.

production of platelets or platelet precursors, useful for treatment of diseases which involve thombocytopenia Thrombopoietic peptides which activate mpl receptors and increase the

Claim 16; Page 62; 91pp; English.

A compound which binds to an mpl receptor comprising a thrombopoietin mimetic poptide (TMP) dimer joined by a linker [TMP\_1-1.[.\_1]\_nTMP\_2], is new. 'NNP\_1 and TMP\_2 are amino acid sequences varying from at least 10 to 14 residues in length comprising x\_2-x\_1-0, x\_2-x\_1-1, x\_2-x\_1-2, X\_2-x\_1-3, x\_2-x\_1-2, x\_1-x\_1-3, and

X\_1-X\_1\_4. X\_1 = 1, A, V, L, S or R; X\_2 = E, D, K or V; X\_3 = G or A; X\_4 = P; X\_5 = T or S; X\_6 = L, I, V, A or F; X\_7 = R or K; X\_8 = Q, N, or E; X\_9 = W, Y or F; X\_1\_0 = L, I, V, A, F, M, or K; X\_1\_1 = A, I, V, L, F, M, or K; X\_1\_2 = A, I, V, L, F, G, S, or Q; X\_1\_3 = R, K, T, V, N, Q or G; X\_1\_4 = A, I, V, L, F, T, R, E, or G; L\_1 = linker occepting 1 to 20 amino acids; and n = 0 or 1. The compounds bind to and activate the c-Mpl receptor which mediates the activity of endogenous thrombopoietin. The TWPs are useful for increasing the production of platelets or platelet precursors (e.g. megakaryocytes) in a mammal, which is useful for treatment of diseases which involve thombocytopenia, e.g. applastic anaemia, immune thrombocytopenia (TFP), human immunodeficiency virus associated ITP, and systemic lupus erythematosus. 

36 AA; Sequence

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Gaps 0; Length 36; Indels Score 179; DB 21; Pred. No. 2e-14; 0; Mismatches 90.9%; nilarity 94.4%; Conservative 0 Query Match Best Local Similarity 34; Matches

; 0

1 IEGPTLRQWLAARAGGGCGGGGGTEGPTLRQWLAARA 36 δŽ

RESULT

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AAB17292 standard; Peptide; 35 AAB17292

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AAB17292;

31-OCT-2000 (first entry)

TPO-mimetic peptide sequence SEQ ID NO:348.

Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cstotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; asthma; thrombosis; pharmaceutical. 

Synthetic.

WO200024782-A2.

04-MAY-2000

99WO-US25044. 25-OCT-1999;

98US-0105371. 23-OCT-1998; 22-OCT-1999;

(AMGE-) AMGEN INC.

Feige U, Liu C, Cheetham J, Boone TC;

WPI; 2000-350702/30.

Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and autoimmune diseases

Example 1; Page 317-318; 608pp; English.

an is: The present invention describes composition of matter (I) comprising a Rc domain, pharmacologically active peptides, and linkers. Where (I) is  $(X1)a \cdot F1 - (X2)b$ , where: F1 = an FC domain; X1 and X2 = ar each independently selected from  $-(L1)c \cdot F1 - (L1)c \cdot P2 - (L3)d \cdot P2 - (L3)d \cdot P3 - (L3)$  us-09-422-838c-33.rag

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independently linkers; and a, b, c, d, e, and f = are each independently of or 1, provided that at least 1 of a and b is 1. The composition can have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are used for producing pharmaceutical compositions. The compositions are use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein a binding, complement fixation, and possibly placental transfer. AAA69443 to AAA69526 and AAB18093 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes composition of matter (I) comprising an FC domain, pharmacologically active peptides, and linkers. Where (I) is: (X1)a-F1-(X2)b, where: F1 = an FC domain; X1 and X2 = are each independently selected from -(Li)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2-(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, P2, P3, and P4 = are each independently sequences of pharmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently
                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; minetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                     1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
                                                                                                                                                                                                                                                                                             Score 177.5; DB 21; Length 35; Pred. No. 2.8e-14;
                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                            1 IEGPTLRQWLAARAGGGGGGGGGGEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                TPO-mimetic peptide sequence SEQ ID NO:350.
                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pharmacologically active peptides, useful autoimmune diseases
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97.28;
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99US-0428082
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                                                                                                                                                                                                                                                                                                                                     35; Conservative
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                                                                                                                                                                                                                                        35 AA;
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                                                                                                                                                                                                                                                                                                   Query Match
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O or 1, provided that at least 1 of a and b is 1. The composition can have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
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[X1)a-Fl-(X2)b, where: Fl = an Fc domain; X1 and X2 = are each independently selected from -(L1)c-Pl-(L1)c-Pl-(L2)d-P2, -(L3)e-P3, or -(L1)c-Pl-(L2)d-P2, -(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3-(L3)e-P3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Modified peptide, therapeutic agent, fusion, Fc domain, cancer, autoimmune disease, cytostatic, antiasthmatic, thrombolytic, VEGF, amunosuppressive, EPO; TPO; CTLA4; mimetic, IL-1; TNF; antagonist, MMP; inhibitor; erythropietin, thrombopoietin, interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     88.6%; Score 174.5; DB 2:
ilarity 94.6%; Pred. No. 6.7e-14;
Conservative 0; Mismatches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 IEGPTLRQWLAARA-GGGCGGGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TPO-mimetic peptide sequence SEQ ID NO:351.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 35; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                          37 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200024782-A2.
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activiles. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69443 to AAA69526 and AAB18955 to AAAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes composition of matter (I) comprising an fee domain, pharmacologically active peptides, and linkers. Where (I) is: (X1)3-F1-(X2)b. where: F1 = an Fc domain, X1 and X2 = are each independently selected from -(L1)c-P1. -(L1)d-P2. -(L3)d-P2. -(L3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMF; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
have cytostatic, antiasthmatic, thrombolytic and immunosuppressive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88.3%; Score 174; DB 21; Length 38; 92.1%; Pred. No. 7.9e-14; Indels 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 IEGPTLRQWLAARA--GGGCGGGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TPO-mimetic peptide sequence SEQ ID NO:360.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; Page 323; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   asthma; thrombosis; pharmaceutical.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cheetham J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99WO-US25044.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 92.1
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      autoimmune diseases -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 38 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200024782-A2.
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be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein half-life, complement fixation, and possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
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activities. DNAs, vectors and host cells from the present invention can
                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; asthma; thrombosis; pharmaceutical.
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                                                                                                                                                                                                                                                                                                                                                                                                                               3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
                                                                                                                                                                                                                                                                                                                                                                      Length 39;
                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                             88.1%; Score 173.5; DB 21;
89.7%; Pred. No. 9.3e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 iegptlrqwlaaragggkpegggggiegptlrqwlaara 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 IEGPTLRQWLAARAGGG----CGGGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TPO-mimetic peptide sequence SEQ ID NO:352.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Boone TC;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB17296 standard; Peptide; 42 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Feige U, Liu C, Cheetham J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99WO-US25044.
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Best Local Similarity 89.7%
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                                                                                                                                                                                                                                                                          39 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200024782-A2.
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                                                                                                                                                                                                                                                                                Sequence
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be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69443 to AAAB16955 to AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
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Sequence 42 AA;

RESULT 27 AAB17291

.B17291 ) AAB17291 standard; Peptide; 34 AA.

AAB17291;

31-OCT-2000 (first entry)

TPO-mimetic peptide sequence SEQ ID NO:347.

Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; auticathmatic; thrombolytic; VEGF; autonomosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; asthma; thrombosis; pharmaceutical.

Synthetic.

WO200024782-A2.

04 - MAY - 2000

25-OCT-1999; 99WO-US25044

23-OCT-1998; 98US-0105371 22-OCT-1999; 99US-0428082

(AMGE-) AMGEN INC

Feige U, Liu C, Cheetham J, Boone TC;

WPI; 2000-350702/30.

Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and autoimmune diseases -

Example 1; Page 317; 608pp; English.

The present invention describes composition of matter (I) comprising an Fc domain, pharmacologically active peptides, and linkers. Where (I) is: (X1)a Fl-(X2)b, where: Fl = an Fc domain, X1 and X2 = are each independently selected from -(L1)c-Pl-(L2)d-P2.

-(L1)c-Pl-(L2)d-P2-(L3)e-P^3, or -(L1)c-Pl-(L2)d-P2-(L3)e-P3-(L4)f-P4 where Pl, P2, P3, and P4 = are each independently sequences of pharmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently or r provided that at least 1 of a and b is 1. The composition can have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cealls from the present invention can be used for producing pharmaceutical compositions. The compositions are

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useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69443 to AAA69526 and AAB18093 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes composition of matter (I) comprising an Fc domain, pharmacologically active peptides, and linkers. Where (I) is: (X1)a-F1-(X2)b, where FI = an Fc domain; X1 and X2 = are each independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2-(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4, where P1, P2, P3, and P4 = are each independently sequences of pharmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The compositions are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases
                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4, minetic; IL-1; TNP; antagonist; MMP; inhibitor; erythropietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                          7
                                                                                                                                                                                   Length 34;
                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                      Pred. No. 1.6e-13;
0; Mismatches 0;
                                                                                                                                                                                       86.8%; Score 171; DB 21;
                                                                                                                                                                                                                                                                                  1 IEGPTLRQWLAARAGGGCGGGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TPO-mimetic peptide sequence SEQ ID NO:346.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Boone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Page 317; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                           AAB17290 standard; Peptide; 33 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cheetham J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99WO-US25044.
                                                                                                                                                                                                      94.48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                          34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-350702/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           autoimmune diseases
                                                                                                                                                                                                        Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200024782-A2.
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                                                                                                                                  Sednence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                AAB17290;
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                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                        RESULT 28
                                                                                                                                                                                                                            Matches
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Page 16

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The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69443 to AAA69526 and AAB186955 to AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FC domain, pharmacologically active peptides, and linkers. Where (I) is:

(X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each

(X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each

(X1)a-F1-(X2)b, where from -(L1)C-F1-(L1)d-F2-(L3)d-F2,

-(L1)C-F1-(L2)d-F2-(L3)e-P3, or -(L1)C-F1-(L2)d-F2-(L3)e-F3-(L4)f-F4

where P1, P2, P3, and P4 = are each independently sequences of

pharmacologically active peptides; L1, L2, L3, and L4 = are each

independently linkers; and a, b, c, d, e, and f = are each independently

o or 1, provided that at least of a and b is 1. The composition can

have cytostatic, antiasthmatic, thrombolytic and immunosuppressive

activities. DNAs, vectors and host cells from the present invention can

be used for producing pharmaceutical compositions. The compositions are

useful for treating cancer, asthma, thrombosis, or autoimmune diseases.

The use of an Fc domain (rather than a Fab domain) can provide a longer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes composition of matter (I) comprising an Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO: TPO; CTLA4; mimetic; IL-1; TNF: antagonist; MMF; inhibitor; erythropoletin; thrombopoletin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and autoimmune diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
                                                                                                                                                                                                                         э;
                                                                                                                                                                                  Length 33;
                                                                                                                                                                                                                           Indels
                                                                                                                                                                                DB 21;
                                                                                                                                                                 Score 164.5; DB 21;
Pred. No. 8.8e-13;
                                                                                                                                                                                                                                                                                    1 iegptlrqwlaarag---ggggiegptlrqwlaara 33
                                                                                                                                                                                                                                                             1 IEGPTLRQWLAARAGGGCGGGGGEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TPO-mimetic peptide sequence SEQ ID NO:354.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; Page 320; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               asthma; thrombosis; pharmaceutical.
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                                                                                                                                                                                                                                                                                                                                                                                                   AAB17298 standard; Peptide; 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cheetham J,
                                                                                                                                                                                83.5%;
91.7%;
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                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-350702/30.
                                                                                                                                                                                Query Match
Best Local Similarity
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                                                                                                                      33 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200024782-A2.
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                                                                                                                        Sequence
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8X866666
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The present invention describes composition of matter (I) comprising an Ec domain, pharmacologically active peptides, and linkers. Where (I) is:

(XI)=F1-(X2)D, Where: F1 = an Fc domain, X1 and X2 = are each independently selected from -{L1}O-FP1-(L2)d-P2.

(L1)C-P1-(L2)d-P2-(L3)e-P^3, or -(L1)C-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, P2, P3, and P4 = are each independently sequences of pharmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently or 1, provided that at least 1 of a and b is 1. The composition can have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention are used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein
                                                                                                                                                                                                                                                                                                                                                     ö
                                       AAA69443
                            A binding, complement fixation, and possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
half-life or incorporate functions such as Fc receptor binding, protein
                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; Immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMF; inhibitor; erythropoietin; thrombopoietin; interleukin, 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
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                                                                                                                                                                                                                                                                                 Length 36;
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                                                                                                                                                                                                                                                                                 21;
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                                                                                                                                                                                                                                                                                                                                                                                                                         36
                                                                                                                                                                                                                                                                                 DB
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                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 IEGPTLRQWLAARAGGGCGGGGGIEGPTLRQWLAARA
                                                                                                                                                                                                                                                                                 Score 159;
Pred. No. 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB17299 standard; Peptide; 36 AA.
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                                                                                                                                                                                                                                                                          80.7%;
ilarity 91.7%;
Conservative
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99US-0428082
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                                                                                                                                                                                                                                                                                                          Local Similarity
nes 33; Conserv
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                                                                                                                                                                          36 AA;
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                                                                                                                                                                                                                                                                                 Query Match
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A binding, complement fixation, and possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A compound which binds to an mpl receptor comprising a thrombopoietin mimetic peptide (TMP) dimer joined by a linker [TMP] ^{-1}(L_1) nTMP] ^{-2}(L_1) is new TMP] and TMP2 are amino acid sequences varying from at least 10 to 14 residues in length comprising X_2 - X_1 = 0, X_2 - X_1 = 1, X_2 - X_1 = 1, X_1 - X_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thrombopoietic peptides which activate mpl receptors and increase the production of platelets or platelet precursors, useful for treatment of diseases which involve thombocytopenia
                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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O
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cyclic or linear thrombopoietin mimetic peptide compound 2.
                                                                                                                                                                                                                                                                                                Score 159; DB 21; Length 36;
                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                        3;
                                                                                                                                                                                                                                                                                                                                            Pred. No. 4.2e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 IEGPTLROWLAARAGGGCGGGGIEGPTLROWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
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/label= linker
23..36
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/label= TMP_1
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/label= TMP_2
                                                                                                                                                                                                                                                                                                80.7%;
91.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99WO-US24834
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                                                                                                                                                                                                                                                                                                                                                                                        33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-365108/31.
                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 33; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (AMGE-) AMGEN INC.
                                                                                                                                                                        36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disulfide-bond
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                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY96521
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T, V, N, Q or G; X_{-1}4 = A, I, V, L, F, T, R, E, or G; L_{-1} = 1 inker comprising 1 to 20 amino acids; and n = 0 or 1. The compounds bind to and activate the c-Mpl receptor which mediates the activity of endogenous thrombopoletin. The TMPs are useful for increasing the production of platelets or platelet precursors (e.g. megakaryocytes) in a mammal, which is useful for treatment of diseases which involve thombocytopenia, e.g. aplastic anaemia, immune thrombocytopenia (ITP), human immunodeficiency virus associated ITP, and systemic lupus erythematosus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes composition of matter (I) comprising an FC domain, pharmacologically active peptides, and linkers. Where (I) is: (X1)a-F1-(X2)b, where FI = an FC domain, X1 and X2 = are each independently selected from -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, -(L3)e-P3-(L3)e-P3-(L4)f-P4 where P1, P2, P3, and P4 = are each independently sequences of pharmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently or I, provided that at least 1 of a and b is 1. The composition can have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can
                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VECF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
                                                                                                                                                                                                                                                                                ;
                                                                                                                                                                                                                                       Length 36;
                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                       Query Match

80.7%; Score 159; DB 21;
Best Local Similarity 91.7%; Pred. No. 4.2e-12;
Matches 33; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                          1 IEGPTLROWLAARAGGGCGGGGIEGPTLROWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TPO-mimetic peptide sequence SEQ ID NO:345.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 1; Page 316; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB17289 standard; Peptide; 32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (AMGE-) AMGEN INC
                                                                                                                                                                                 36 AA;
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be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes composition of matter (I) comprising an (X1)a-F1-(X2)b, where: F1 = an FC domain, X1 and X2 = are each independently selected from -(L1)c-F1-(L2)d-F2, -(L3)c-F2,-(L3)c-F2,-(L3)c-F2,-(L3)c-F2,-(L3)c-F2,-(L3)c-F2,-(L3)c-F2,-(L3)c-F2,-(L3)c-F3, and P4 = are each independently sequences of pharmacologically active peptides; L1, L2, L3, and L4 = are each independently sequences of or 1, provided that at least 1 of a and b is 1. The composition can have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are
                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autofimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO. TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoletin; thrombopoletin; interleukin 1; vyctotoxic T cell Jymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and autoimmune diseases -
                                                                                                                                                                                                                                                 4
                                                                                                                                                                                                          Score 158; DB 21; Length 32;
Pred. No. 4.9e-12;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                  1 iegptlrqwlaara----ggggiegptlrqwlaara 32
                                                                                                                                                                                                                                                                                  1 IEGPTLRQWLAARAGGGCGGGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TPO-mimetic peptide sequence SEQ ID NO:356.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; Page 321; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                               AAB17300 standard; Peptide; 36 AA
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                                                                                                                                                                                                      80.2%;
88.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                  Query Match
Best Local Similarity 88.9°
Matches 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-350702/30.
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                                                                                                                                                    32 AA;
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                                                                                                                                                      Sequence
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useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69443 to AAA69526 and AAB180913 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thrombopoietic peptides which activate mpl receptors and increase the production of platelets or platelet precursors, useful for treatment of diseases which involve thombocytopenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A compound which binds to an mpl receptor comprising a thrombopoietin mimetic peptide (TMP) dimer joined by a linker [TMP]-(L_1)_nTMP_2], is new, TMP_1 and TMP_2 are amino acid sequences varying from at least 10 to 14 residues in length comprising X_2-X_1_0, X_2-X_1_1, X_2-X_1_2, X_2-X_1_3, X_2-X_1_4, X_1-X_1-X_1, 0, X_1-X_1-1, X_1-X_1-2, X_1-X_1-3, and X_1-X_1-4, X_1-1-1, X_1-X_1-2, X_1-X_1-3, and X_4-P; X_5=T or S; X_6=L, I, V, A or F; X_7=R or K; X_8=Q, N, or E; X_9=W, X or F; X_1-0=L, I, V, A, F; W, or K; X_1-1=A, I, V,
                                                                                                                                                                                           Gaps
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "optionally linked to an Fc molecule"
                                                                                                                                                              36;
                                                                                                                                                                                           Indels
                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                                                                                                          Linear thrombopoietin mimetic peptide compound 3.
                                                                                                                                                            Score 157; DB 21;
Pred. No. 7.2e-12;
                                                                                                                                                                                                                        36
                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                      1 IEGPTLRQWLAARAGGGCGGGGIEGPTLRQWLAARA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= TMP_1
15..22
/label= linker
                                                                                                                                                                                                                                                                                                                               AAY96522 standard; peptide; 36
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/label= TMP_2
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                                                                                                                                                         79.78;
91.78;
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                                                                                                                                                                                           Conservative
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                                                                                                                                                                         Best Local Similarity
Matches 33; Conserv
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                                                                                                             36 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200024770-A2
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Modified-site
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                                                                                                             Sequence
                                                                                                                                                            Query Match
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L, F, S, T, K, H, or E; x_{-1} = A, I, V, L, F, G, S, or Q; x_{-1} = R, K, T, V, N, Q or G; x_{-1} 4 = A, I, V, L, F, T, R, E, or G; L_{-1} = linker comprising 1 to 20 amino acids; and n = 0 or 1. The compounds bind to and activate the C-Mpl receptor which mediates the activity of endogenous thrombopoietin. The TMPs are useful for increasing the production of platelets or platelet precursors (e.g. megakaryozyctes) in a mammal, which is useful for treatment of diseases which involve thombocytopenia e.g. aplastic anaemia, immune thrombocytopenia (ITP), human immunodeficiency virus associated ITP, and systemic lupus erythematosus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79.7%; Score 157; DB 21;
91.7%; Pred. No. 7.2e-12;
Live 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 IEGPTLRQWLAARAGGGCGGGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TPO-mimetic peptide sequence SEQ ID NO:344.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Page 316; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB17288 standard; Peptide; 31 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Feige U, Liu C, Cheetham J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99WO-US25044.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              autoimmune diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-350702/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (AMGE-) AMGEN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200024782-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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Fc domain, pharmacologically active peptides, and linkers. Where (I) is: (X1)a-F1-(X2)b, where F1 = an Fc domain; X1 and X2 = are each independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2, -(L3)e-P2, -(L3
                      be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes composition of matter (1) comprising an FC domain, pharmacologically active peptides, and linkers. Where (1) is:
activities. DNAs, vectors and host cells from the present invention can
                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VBGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin; vascular cell lymphocyte antigen 4; tumour necrosis factor; vascular endotheilal growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                            5,
                                                                                                                                                                                                                                                                                                                                                                   Score 151.5; DB 21; Length 31;
                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 2.7e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 IEGPTLRQWLAARAGGGCGGGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TPO-mimetic peptide sequence SEQ ID NO:343.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 1; Page 315-316; 608pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA.
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB17287 standard; Peptide; 30
                                                                                                                                                                                                                                                                                                                                                                      76.9%;
86.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99WO-US25044.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      31; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
                                                                                                                                                                                                                                                                                      31 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200024782-A2.
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                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
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be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an FC domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as FC receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                         Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLAA; mimetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                           .
9
                                                                                                                                                                 Length 30;
                                                                                                                                                                                          Indels
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0
                                                                                                                                                         73.6%; Score 145; DB 21;
83.3%; Pred. No. 1.5e-10;
1ve 0; Mismatches 0;
                                                                                                                                                                                                                1 IEGPTLRQWLAARAGGGCGGGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                TPO-mimetic peptide sequence SEQ ID NO:353.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 1; Page 320; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                             AAB17297 standard; Peptide; 32 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Feige U, Liu C, Cheetham J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99WO-US25044.
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99US-0428082.
                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                        Best Local Similarity 83.3
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             autoimmune diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-350702/30.
                                                                                                                 30 AA;
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                                                                                                                   Sequence
                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                           AAB17297;
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                                                                                                                                                                                                                                                                                    RESULT
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The present invention describes composition of matter (I) comprising an Cx domain, pharmacologically active peptides, and linkers. Where (I) is: (X1)a-F1-(X2)b, where: F1 = an FC domain; X1 and X2 = are each independently selected from -(LL)c-P1-(LL)d-P2.

-(LL)c-P1-(L2)d-P2-(L3)e-P^3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, P2, P3, and P4 = are each independently sequences of pharmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently independently linkers; and a b, c, d, e, and f = are each independently or 1, provided that at least 1 of a and b is 1. The composition can have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are

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useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an FC domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as FC receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thrombopoietin; mimetic; TMP; TPO; platelet; megakaryocyte; production; anti-human immunodeficiency virus; anti-HIV; anti-anemic; dermatological; immunosuppressive; anti-inflammatory; linker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thrombopoietic peptides which activate mpl receptors and increase the production of platelets or platelet precursors, useful for treatment of diseases which involve thombocytopenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A compound which binds to an mpl receptor comprising a thrombopoietin mimetic peptide (TMP) dimer joined by a linker [TMP_1-(L_1)_nTMP_2], is new TMP_1 and TMP_2 are amino acid sequences varying from at least 10 to 14 residues in length comprising X_2 - X_1 - I_0, X_2 - X_{1-1}, X_2 - X_{1-1}, X_2 - X_{1-2}, X_1 - X_1 - I_1, X_1 - X_1 - I_2, X_1 - X_1 - I_3, and X_1 - X_1 - I_4, X_1 - X_1 - I_2, X_1 - X_1 - I_3, and X_1 - X_1 - I_4, X_1 - I_4, X_1 - I_5, X_1 - I_5, X_2 - I_5, X_1 - I_5, X_2 - I_5, X_3 - I_5, and X_1 - I_4 - I_5, X_1 - I_5, X_2 - I_5, X_3 - I_5, X_3 - I_5, and
                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                          4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "optionally linked to an Fc molecule"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "optionally linked to an Fc molecule"
                                                                                                                                                                     73.1%; Score 144; DB 21; Length 32; 83.3%; Pred. No. 2.1e-10;
                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                         1 IEGPTLRQWLAARAGGGCGGGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thrombopoletin mimetic peptide compound 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                       ¥
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 16; Page 61; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                AAY96520 standard; peptide; 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15..18
/label= linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19..32
/label= TMP_2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= TMP_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cheetham J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98US-0105348
                                                                                                                                                                                                                                                                                                                                                                                                              04-SEP-2000 (first entry)
                                                                                                                                                                                                   Conservative
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                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                    32 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (AMGE-) AMGEN INC.
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                                                                                                                    Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide
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                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                   AAY96520
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1;
X_-4 = P; X_-5 = T or S; X_-6 = L, I, V, A or F; X_-7 = R or K; X_-11 = A, I, V, L, F, S, T, K, H, Or E; X_-12 = A, I, V, A, F, M, or K; X_-11 = A, I, V, L, F, S, T, K, H, Or E; X_-12 = A, I, V, L, F, T, R, E, Or G; L_-1 = 1 inker comprising 1 to 20 amino acids; and n = 0 or 1. The compounds bind to activate the c-Mpl receptor which mediates the activity of endogenous thrombopoietin. The TMPs are useful for increasing the production of platelete precursors (e.g. megakaryocytes) in a mammal, which is useful for treatment of diseases which involve thombocytopenia, e.g. aplastic anaemia, immune thrombocytopenia (ITP), human immunodeficiency virus associated ITP, and systemic lupus erythematosus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thrombopoietin; mimetic; TMP; TPO; platelet; megakaryocyte; production; anti-human immunodeficiency virus; anti-HIV; anti-anemic; dermatological; immunosuppressive; anti-inflammatory; linker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thrombopoietic peptides which activate mpl receptors and increase the production of platelets or platelet precursors, useful for treatment of diseases which involve thombocytopenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A compound which binds to an mpl receptor comprising a thrombopoietin mimetic peptide (TMP) dimer joined by a linker [TMP_1-(L_1)_nTMP_2], is new. TMP_1 and TMP_2 are amino acid sequences varying from at least
                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                              4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note= "optionally linked to an Fc molecule"
                                                                                                                                                                                                                                              Length 32;
                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                              Score 144; DB 21;
Pred. No. 2.1e-10;
                                                                                                                                                                                                                                                                                                              1 IEGPTLRQWLAARAGGGCGGGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                        1 iegptlrqwlaara---gpngiegptlrqwlaara 32
                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thrombopoietin mimetic peptide compound 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                        AAY96527 standard; peptide; 34 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 16; Page 64; 91pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17..20
/label= linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21..34
/label= TMP_2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3..16
/label= TMP_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Liu C, Feige U, Cheetham J;
                                                                                                                                                                                                                                                73.1%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99WO-US24834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98US-0105348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-SEP-2000 (first entry)
                                                                                                                                                                                                                                                                 Best Local Similarity 83.3
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-365108/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (AMGE-) AMGEN INC.
                                                                                                                                                                                                    32 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200024770-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY96527;
                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide
                                                                                                                                                                                                                                                                                                                                                                                            39
                                                                                                                                                                                                                                                                                                                                                                                                              AAY96527
                                                                                                                                                                                                                                                                                                                                                                                            RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                             QQ
             2222222222222X8
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The present invention describes composition of matter (I) comprising an Fc domain, pharmacologically active peptides, and linkers. Where (I) is: (x1)a+F(x2)b, where: Fl = an Fc domain; X1 and X2 = are each independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2, -(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4
                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                        Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMF; inhibitor; erythropoletin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                         4;
                                                                                                                                                                                                                 Length 34;
                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel composition of matter comprising an Fc domain and
                                                                                                                                                                                                                 Score 144; DB 21;
Pred. No. 2.3e-10;
0; Mismatches 2;
                                                                                                                                                                                                                                                                1 IEGPTLRQWLAARAGGGCGGGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                               3 iegptlrqwlaara---gpngiegptlrqwlaara
                                                                                                                                                                                                                                                                                                                                                                                                                      TPO-mimetic peptide sequence SEQ ID NO:342.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; Page 315; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                  AAB17286 standard; Peptide; 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Feige U, Liu C, Cheetham J,
                                                                                                                                                                                                                    73.1%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99WO-US25044.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98US-0105371.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-0428082
                                                                                                                                                                                                                                                                                                                                                                                                31-OCT-2000 (first entry)
                                                                                                                                                                                                                                 Best Local Similarity 83.3
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   autoimmune diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-350702/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (AMGE-) AMGEN INC.
                                                                                                                                                                                    Sequence 34 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200024782-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-MAY-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                                                                                           AAB17286;
                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                             RESULT 40
                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                        AAB17286
                                                                                                                                                                                                                                                                                                                                                                          δ
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where Pl, P2, P3, and P4 = are each independently sequences of pharmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, C, d, e, and f = are each independently linkers; and a, b, C, d, e, and f = are each independently of or 1, provided that at least 1 of a and b is 1. The composition can have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69443 sequences used in the exemplification of the present invention.
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29 AA; Sequence

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Gaps
                                       7;
                DB 21; Length 29;
                                       Indels
Score 138.5; DB 21,
                                                        1 IEGPTLRQWLAARAGGGGGGGGGEGPTLRQWLAARA 36
                                                                               1 iegptlrqwlaara----giegptlrqwlaara 29
                          Pred. No. 8.56
0; Mismatches
             70.3%;
80.6%;
           Ouery Match 70.31
Best Local Similarity 80.65
Matches 29; Conservative
                                                          ò
                                                                                 a
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AAB17285 standard; Peptide; 28 31-OCT-2000 (first entry) AAB17285: 41 AAB17285 

Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytocoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; asthma; thrombosis; pharmaceutical. TPO-mimetic peptide sequence SEQ ID NO:341.

Synthetic.

WO200024782-A2.

04-MAY-2000

99WO-US25044. 25-OCT-1999;

98US-0105371 99US-0428082 23-OCT-1998; 22-OCT-1999;

(AMGE-) AMGEN INC.

Boone TC; Feige U, Liu C, Cheetham J,

WPI; 2000-350702/30.

Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and autoimmune diseases

Example 1; Page 315; 608pp; English.

The present invention describes composition of matter (I) comprising an Ec domain, pharmacologically active peptides, and linkers. Where (I) is:  $(x,1)a+\Gamma(x,2)b$ , where:  $\Gamma = an$  FC domain, X1 and X2 = ar each independently selected from  $-(L1)c-\Gamma 1 - (L2)d-P2$ ,  $-(L1)c-\Gamma 1 - (L2)d-P2$ , and P4 = ar each independently sequences of

pharmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently linkers; and a, b, c, d, e, and f = are each independently have cytostatic, antiasthmatic, if a and b is 1. The composition can be used for producing pharmaceutical compositions. The compositions are useful for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer The use of moreoperate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention. 8.5566666666666555

28 AA; Sequence

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8; Gaps
67.0%; Score 132; DB 21; Length 28; 77.8%; Pred. No. 4.7e-09;
                           Indels
                           ;
;
                                                 1 IEGPTLROWLAARAGGCCGGGGIEGPTLROWLAARA 36
                                                                    Mismatches
                          ;
0
                          Conservative
            Local Similarity
nes 28; Conserv
 Query Match
                      Matches
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RESULT 42 AAB16970

Ob ŏ

AAB16970 standard; Peptide; 29 AA.

AAB16970;

31-OCT-2000 (first entry)

TPO-mimetic peptide sequence SEQ ID NO:26.

Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; asthma; thrombosis; pharmaceutical. 

Synthetic.

WO200024782-A2.

04-MAY-2000

99WO-US25044. 25-OCT-1999;

98US-0105371. 99US-0428082. 23-OCT-1998; 22-OCT-1999;

(AMGE-) AMGEN INC.

Cheetham J, Boone TC; Feige U, Liu C,

WPI; 2000-350702/30.

Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and autoimmune diseases

Claim 19; Page 204; 608pp; English.

an is: The present invention describes composition of matter (I) comprising a Fc domain, pharmacologically active peptides, and linkers. Where (I) i (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each independently selected from -(L1)c-P1-(L1)c-P1-(L3)d-P2. -(L1)c-P1-(L2)d-P2-(L3)e-P2-(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-

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independently linkers; and a, b, c, d, e, and f = are each independently of or 1, provided that at least 1 of a and b is 1. The composition can have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69443 to AAA69526 and AAB18031 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
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Sequence

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Gaps
                           7;
  21; Length 29;
                           1; Indels
  Score 131.5; DB 2. Pred. No. 5.6e-09;
                                                  1 IEGPTLRQWLAARAGGGCGGGGIEGPTLRQWLAARA 36
                          0; Mismatches
 66.8%;
                          28; Conservative
Query Match
Best Local Similarity.
                           Matches
                                                  ò
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1 iegptlrqwlaara----xieqptlrqwlaara 29 g

AAB16973 standard; Peptide; 31 AA 31-OCT-2000 AAB16973; AAB16973 RESULT

PPO-mimetic peptide sequence SEQ ID NO:29. (first entry) 

autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP: inhibitor; erythropoletin; thrombopoletin; interleukin 1; cyttotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; asthma; thrombosis; pharmaceutical. Modified peptide; therapeutic agent; fusion; Fc domain; cancer;

Synthetic.

WO200024782-A2.

99WO-US25044. 25-OCT-1999; 34 - MAY - 2000

98US-0105371 99US-0428082 22-OCT-1999; 23-OCT-1998;

(AMGE-) AMGEN INC.

Feige U, Liu C, Cheetham J, WPI; 2000-350702/30.

Boone TC;

Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and autoimmune diseases -

Claim 19; Page 205; 608pp; English.

The present invention describes composition of matter (I) comprising an FC domain, pharmacologically active peptides, and linkers. Where (I) is: (X1)a-FI-(X2)b, where: FI = an FC domain; X1 and X2 = are each independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-(L2)d-P2-(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, P2, P3, and P4 = are each independently sequences of pharmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently

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Ξ.
O or 1, provided that at least 1 of a and b is 1. The composition can have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes composition of matter (I) comprising an Pre domain, pharmacologically active peptides, and linkers. Where (I) is: (X1)a \cdot F1 - (X2)b, where: F1 = an Fc domain, X1 and X2 = are each independently selected from -(L1)c-P1, -(L2)d-P2, -(L3)d-P2, -(L3)d-P2, -(L3)d-P2, -(L3)d-P2, -(L3)d-P2, -(L3)d-P2, -(L3)d-P2, -(L3)d-P3, and P4 = are each independently sequences of pharmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently 0 or 1, provided that at least 1 of a and b is 1. The composition can
                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGP; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
                                                                                                                                                                                                                                                                                                                                .
2
                                                                                                                                                                                                                                                                                        DB 21; Length 31;
                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                3,
                                                                                                                                                                                                                                                                                                               Pred. No. 1e-08
                                                                                                                                                                                                                                                                                                                                                                      1 IEGPTLRQWLAARAGGGCGGGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                            1 iegptlrqwlaara----xkxiegptlrqwlaara 31
                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                        65.7%; Score 129.5; 77.8%; Pred. No. 1e-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TPO-mimetic peptide sequence SEQ ID NO:30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Boone TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 19; Page 205-206; 608pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB16974 standard; Peptide; 31 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Liu C, Cheetham J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99WO-US25044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98US-0105371
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-350702/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    autoimmune diseases
                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (AMGE-) AMGEN INC.
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                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB16974;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Feige U,
                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                             Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB16974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
        888888888888888888
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have cytostatic, antiasthmatic, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, astbma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibily placental transfer. AAA69443 to AAA69526 and AAB18033 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes composition of matter (I) comprising an FC domain, pharmacologically active peptides, and linkers. Where (I) is: (X1)a-F1-(X2)b, where: F1 = an FC domain; X1 and X2 = are each independently selected from -(L1)C-P1, -(L1)C-P1-(L2)d-P2, -(L3)d-P2, -(L3)d-P2, -(L3)d-P2, -(L3)d-P2, -(L3)d-P2, -(L3)d-P2, -(L3)d-P3, or -(L1)C-P1-(L2)d-P2, -(L3)d-P3, or -(L1)C-P1-(L2)d-P2, -(L3)d-P3, or -(L1)C-P1-(L2)d-P2, -(L3)d-P3, or -(L1)C-P1, -(L3)d-P3, -(L4)d-P4, or -(L3)d-P3, or -(L3)d-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 21; Length 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65.7%; Score 129.5; DB 77.8%; Pred. No. 1e-08; Live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 IEGPTLRQWLAARAGGGCGGGGIEGPTLRQWLAARA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 iegptlrqwlaara----xkxiegptlrqwlaara 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TPO-mimetic peptide sequence SEQ ID NO:27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Boone TC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    asthma; thrombosis; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB16971 standard; Peptide; 29 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99WO-US25044
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99US-0428082
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 77.89
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-350702/30.
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                                                                                                                                                                                                                                                                                                                                                                      31 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-OCT-1998;
22-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-MAY-2000
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activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AAA69443 to AAA869526 and AAB18093 represent nucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                    7;
                                                                                                                                                                                                                                                                                     63.7%; Score 125.5; DB 21; Length 29; 72.2%; Pred. No. 2.8e-08;
                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                             2; Mismatches
                                                                                                                                                                                                                                                                                        Query Match 63.77
Best Local Similarity 72.23
Matches 26; Conservative
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